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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:     January  6, 2004, 23:20:54 ; Search time 922 Seconds
                                          (without alignments)
                                10399.570 Million cell updates/sec

Title:          US-09-750-240-10
Perfect score:  3552
Sequence:       1 atgtcatggttagtggcct.........aagggaccaaggtggcact 3552

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:    5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB Length	ID	Description		Score	Pred.		ID
1	3552	100.0	3552	22	AAD08567	Human cardiac aden
2	3552	100.0	3552	24	ABS54137	Human cDNA encodin
3	3545.6	99.8	4942	20	AAX00461	Human type VI aden
4	3484.8	98.1	3549	22	AAD08563	Human cardiac aden
5	3484.8	98.1	3549	24	ABS54133	Human cDNA encodin
6	3443.2	96.9	3582	22	AAD08568	Human modified car
7	3443.2	96.9	3582	24	ABS54138	Chimaeric cDNA enc
8	3057.6	86.1	4046	14	AAQ42525	Cardiac adenylyl c

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 9  2816.2  79.3  5841  24  ABI99680    Mouse ischaemic co
10  2810.4  79.1  4131  21  AAA53923    Type VI adenylyl c
11  1763.4  49.6  1812  22  AAD08562    Human partial card
12  1763.4  49.6  1812  24  ABS54132    Human cDNA encodin
13  1763.4  49.6  2127  19  AAV23246    Human adenylylcycl
14   1761   49.6  4523  20  AAX00462    Human type V adeny
15  1750.8  49.3  4356  16  AAQ95540    Cardiac adenylyl c
16  1749.2  49.2  4356  14  AAQ37543    Cardiac adenylyl c
17  1696.2  47.8  3924  21  AAA53922    Type V adenylyl cy
18   886.2  24.9  3137  24  AAD28058    Human adenylyl and
19   604.4  17.0  3978  21  AAA53918    Adenylyl cyclase t
20   590.8  16.6   837  22  AAS30177    DNA encoding rena
21    542   15.3  3811  24  AAD28061    Human adenylyl and
22   528.6  14.9   915  22  AAS30223    DNA encoding rena
23   528.6  14.9   915  22  AAS27146    cDNA encoding nove
24   512.4  14.4  3518  22  AAS02694    Human adenylate cy
25    510   14.4  6005  25  ABX10417    DNA encoding prote
26   498.6  14.0  6470  24  AAD31191    Human adenylate cy
27    497   14.0  4011  22  AAD06820    Human adenylate cy
28    493   13.9  6196  24  AAD41270    Human adenylate cy
29   492.4  13.9  3243  24  AAD41265    Human adenylate cy
30   485.2  13.7  4601  21  AAA53925    Type VIII adenylyl
31   476.6  13.4  4827  23  ABL07501    Drosophila melanog
32   474.8  13.4  5873  24  AAD31190    Human adenylate cy
33   465.8  13.1  3769  24  AAD28057    Human adenylyl and
34   458.6  12.9  4008  17  AAT14528    Rat adenylyl cycla
35   458.6  12.9  4008  21  AAA53919    Adenylyl cyclase t
36   456.2  12.8  2731  25  ACA56746    Signalling pathway
37   456.2  12.8  3312  24  ABN89298    Human adenylate cy
38   455.4  12.8  4533  21  AAA53920    Type III adenylyl
39   449.4  12.7  5199  21  AAA53924    Type VII adenylyl
40    431   12.1  3357  21  AAA53921    Type IV adenylyl c
41   424.8  12.0  4355  24  ABL39754    Human NS cDNA sequ
42   416.8  11.7  3505  24  AAD34078    Human secreted pro
43   408.2  11.5  2601  21  AAC99124    Human pancreatic c
44   399.6  11.2  4080  22  AAH16647    Human cDNA sequenc
45   389.8  11.0  1652  21  AAA53926    Adenylyl cyclase C
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ALIGNMENTS

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RESULT 1
AAD08567
ID   AAD08567 standard; DNA; 3552 BP.
XX
AC   AAD08567;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human cardiac adenylcyclase VI (ACVI) isoform #2 DNA.
XX
KW   Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW   myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW   adenylylcyclase; adenylate cyclase; cAMP synthetase;
KW   G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW   cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3507
FT                   /*tag= a
FT                   /product= "Human cardiac adenylcyclase VI isoform #2"
FT                   /EC_number= "4.6.1.1"
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PN   WO200148164-A2.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US35411.
XX
PR   27-DEC-1999;  99US-0472667.
```

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XX
PA  (REGC ) UNIV CALIFORNIA.
XX
PI  Hammond HK, Gao M;
XX
DR  WPI; 2001-418260/44.
DR  P-PSDB; AAE04311.
XX
PT  Novel polynucleotide encoding a modified adenylylcyclase polypeptide
PT  useful for enhancing cardiac function in mammalian hearts, and for
PT  treating heart disease, especially congestive heart failure -
XX
PS  Claim 6; Page 134-140; 153pp; English.
XX
CC  The present invention relates to methods and compositions for enhancing
CC  cardiac function in mammalian hearts by inserting transgenes encoding
CC  beta-adrenergic signalling proteins (beta-ASP) which increase
CC  beta-adrenergic responsiveness within the myocardium using in vivo
CC  gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC  receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase,
CC  adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC  (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC  in mammalian hearts and for treating heart disease, especially
CC  congestive heart failure. The present DNA sequence encodes human
CC  cardiac adenylylcyclase VI (ACVI) isoform which is used for generating
CC  a fourth beta-ASP transgene, used in the exemplification
CC  of the invention.
XX
SQ  Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Query Match     100.0%;   Score 3552;   DB 22;   Length 3552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3552;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Qy      1 ATGTCATGGTTTAGTGGCTTCCTGTCCTAAAGTGGATGAAACGGAAAACAGCCTGGGGT  60
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Db      1 ATGTCATGGTTTAGTGGCTTCCTGTCCTAAAGTGGATGAAACGGAAAACAGCCTGGGGT  60

Qy     61 GAACGCAATGGCAGAAGCGTTCGCTCCGGATGCAGAGCCACCCAGCGCCCCGGGGCCCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAACGCAATGGCAGAAGCGTTCGCTCCGGATGCAGAGCCACCCAGCGCCCCGGGGCCCC 120

Qy    121 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCGCCCCGGGGCCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCGCCCCGGGGCCCC 180

Qy    181 CCTCGGTGCCCCTGGCCAGGATGACGGCCTTCATCCGGAGGGGCGGCCAGGCAAG 240
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Qy    241 GAGCTGGGCGCGGGCAGTGCGGGCAGTGCCCTTCGGGCTTCGAGGATACCGAGGTGACAACGACCAGCG 300
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Qy    301 GGCGGGACGGCGGCTGAGGTGGGCGCCCCAGGAGTGGGCGATCCTGCTGCGGC 360
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Qy    361 CGTCTGGTGTCGCAGGGTGTCAGTGCGAAGCAGTTCCGTTCGGCAAGCTGATGAGCGCGTCGGCGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGTCTGGTGTCGCAGGGTGTCAGTGCGAAGCAGTTCCGTTCGGCAAGCTGATGAGCGCGTCGGCGC 420

Qy    421 CAGCGGGTACTTCTTCCAGATGAACCAGAGCAGCTGAACGCTGATGTGCTGCTGGTG 480
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Qy    481 CTGCTCACAGGGGTGCTGGCTTTCCACGCCGCACCCGCACCCGCCCTCAGCCTGCCTAT 540
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Qy    541 GTGGGACTGTTGGCCGCGGCCCGCCCGCCCTGTTCGTGGGGCTTCATGTGGGTTGTGTAACCGG 600
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Qy    661 GCAGTGCAGGTCGGGGCGCGCTTCGGCAGCGACAGACCCGGCAGCCCTCGGGCGGCCTCGG 720
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Qy    721 TGCCCTGTGTCTTGTCTACATCGCCTACATCGCCTACATCGCCTACATCGCCTACACGCTGCC 780
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Db    721 TGCCCTGTGTCTTGTCTACATCGCCTACATCGCCTACATCGCCTACATCGCCTACACGCTGCC 780

Qy    781 GTCCTCAGCGGCCTGGCCTTCCACCTTGCATTGATCTTGGCTGGCAACTAACCGT 840
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Qy    841 GGTGATGCCTTCCTCGGAAGCAGCTCGGTGCCAATGTGCTGCTTCCTCTGCACCAAC 900
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Qy    901 GTCATTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
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Qy   1081 AAAAAGAAGACATGATGTTCCACAAGATCTACATACAAGAGCATGACAATGTCAGCATC 1140
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Qy 2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACACGGGAGGAAGGAGATGGAGGAGGAGCTA 2820
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Qy 2821 CAGGCATACAACCGGAGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2880
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Qy 2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTCATGTGGAGCTGGAGGACAAACAATGAG 3000
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Db 2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTCATGTGGAGCTGGAGGACAAACAATGAG 3000

Qy 3001 GGTGTCGAGTGCTTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 GGTGTCGAGTGCTTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060

Qy 3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTAGACCTACATGGCTGCC 3120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTAGACCTACATGGCTGCC 3120

Qy 3121 TCAGGGCTGAACGGCCAGCAACCTACAGGTGGGCCGCTCCCCACTACTCGCCCTGGCT 3180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 TCAGGGCTGAACGGCCAGCAACCTACAGGTGGGCCGCTCCCCACTACTCGCCCTGGCT 3180

Qy 3181 GACTACGGCCATGCGGCTCAGTGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 GACTACGGCCATGCGGCTCAGTGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240

Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTCATCGGGGGTCTCGG 3300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTCATCGGGGGTCTCGG 3300

Qy 3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360

Qy 3361 GGGGTCCCCGACCGAATCCAGGTGACCGACCTGTGACGGTTCTGCCAAGGGC 3420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3361 GGGGTCCCCGACCGAATCCAGGTGACCGACCTGTGACGGTTCTGCCAAGGGC 3420

Qy 3421 TACCAGCTGGAGTGTCGAGGGGTGTCAAGGTGACCACTAC 3480
        ||||||||||||||||||||||||||||||||||||||||
Db 3421 TACCAGCTGGAGTGTCGAGGGGTGTCAAGGTGACCACTAC 3480

Qy 3481 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGACCACAAATTCAGCTGAAGGGACC 3540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGACCACAAATTCAGCTGAAGGGACC 3540

Qy 3541 AAGGTGGGCACT 3552
        ||||||||||||
Db 3541 AAGGTGGGCACT 3552

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FH   Key             Location/Qualifiers
FT   CDS             1..3507
FT                   /*tag= a
FT                   /EC_number= "4.6.1.1"
FT                   /product= "Adenylycyclase isoform 6"
XX
PN   US2002103147-A1.
XX
PD   01-AUG-2002.
XX
PF   26-DEC-2000; 2000US-0750240.
XX
PR   27-DEC-1999;  99US-0472667.
XX
PA   (HAMM/)  HAMMOND H K.
PA   (INSE/)  INSEL P A.
PA   (PING/)  PING P.
PA   (POST/)  POST S R.
PA   (GAOM/)  GAO M.
XX
PI   Hammond HK, Insel PA, Ping P, Post SR, Gao M;
XX
DR   WPI; 2002-690626/74.
DR   P-PSDB; ABG32869.
XX
PT   Enhancing cardiac function in a mammal for treating heart disease such
PT   as congestive heart failure, by delivering to the heart of the mammal a
PT   vector comprising a gene encoding a beta-adrenergic signalling protein
PT   -
XX
PS   Claim 22; Page 42-44; 69pp; English.
XX
CC   The invention relates to enhancing cardiac function in a mammal,
CC   involves delivering a vector to the heart of the mammal, where the
CC   vector comprises a gene encoding a beta-adrenergic signalling protein
CC   (beta-ASP) e.g. adenylycyclase isoform 6 (AC-VI) operably linked to a
CC   promoter. Generating a recombinant replication-defective viral particle
CC   involves introducing first and second plasmids into a replication-
CC   permissive mammalian cell expressing one or more adenovirus genes
CC   conferring replication competence, where the first plasmid comprises a
CC   gene encoding a beta-ASP operably linked to a promoter and further
CC   comprises a replication-defective human adenovirus genome, and the second
CC   plasmid comprises a replication-proficient human adenovirus genome and
CC   further comprises an additional polynucleotide sequence making the second
CC   plasmid too large to be encapsidated in an adenovirus particle, where
CC   rescue recombination takes place between the first plasmid and the second
CC   plasmid to generate a recombinant adenoviral genome comprising the gene
CC   encoding a beta-ASP but lacking one or more adenoviral replication genes,
CC   where the recombinant genome is sufficiently small to be encapsidated in
CC   an adenovirus particle, identifying successful recombinant viral vectors
CC   in cell culture, and propagating a resulting recombinant viral particle
CC   in replication-permissive mammalian cells expressing the missing
CC   adenoviral replication genes to generate a recombinant replication-
CC   defective viral particle. The method is useful for enhancing cardiac
CC   function in a mammal, preferably human and is specifically useful for
CC   treating heart diseases such as congestive heart failure (CHF).
CC   The present sequence is a cDNA encoding human Adenylylcyclase
CC   isoform 6, AC-VI, a beta-ASP, used in the method of the invention.
XX
SQ   Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;
```

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Query Match             100.0%;  Score 3552;  DB 24;  Length 3552;
Best Local Similarity   100.0%;  Pred. No 0;
Matches 3552;   Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCATGGTTTAGTGGCCTTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT     60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCATGGTTTAGTGGCCTTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT     60

Qy         61 GAACGGCAATGGCAGAAGCGTTCGCGGCGCGGCCGTGCGGCACTCGGCGCAGGTGGCTTCTGCACG    120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2281 ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 CCTGCTGACATCACTGCCTGCCACCTGCCACCTGCGAGCAGCTGCAATTACTCTCTGGGATGCT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CCTGCTGACATCACTGCCTGCCACCTGCCACCTGCGAGCAGCTGCAATTACTCTCTGGGATGCT 2400

Qy  2401 CCCTGTGTGAGGGCACCATGCCACCTGCGAGTACTTCATCGGGAACATG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CCCTGTGTGAGGGCACCATGCCACCTGCGAGTACTTCATCGGGAACATG 2460

Qy  2461 CTGCTGAGTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2521 ATGATCTTTGTCTTGTGGGGCTCATCTATTTGGTGTGCTCCCCAGCCACC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 ATGATCTTTGTCTTGTGGGGCTCATCTATTTGGTGTGCTCCCCAGCCACC 2580

Qy  2581 ATCTTTGACAACTATGACCTTACTGCTTGGGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 ATCTTTGACAACTATGACCTTACTGCTTGGGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2640

Qy  2641 TTTGATGGGCTGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCGTG 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTTGATGGGCTGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCGTG 2700

Qy  2701 ATTCTGCTGTGTTTGCGGTGGGCGCTGTATCTGCAGCAGGTGAGTGGACTGCC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 ATTCTGCTGTGTTTGCGGTGGGCGCTGTATCTGCAGCAGGTGAGTGGACTGCC 2760

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCCAACAGGGAGAAGGAGGAGATGGGAGGAGCTA 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCCAACAGGGAGAAGGAGGAGATGGGAGGAGCTA 2820

Qy  2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGGCGGCCCACTTC 2880
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Qy  2881 CTGGCCCGGAGCGGCCGGTTCCCGCAGCTGGAAATGATGAACTCTACTATCAGTCGTGTGGCTGTT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCAAACAATGAG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCAAACAATGAG 3000

Qy  3001 GGTGTCGAGTGCCTGCGGCCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 GGTGTCGAGTGCCTGCGGCCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060

Qy  3061 GAGGAGCCGGTTCCCGCAGCTGGAAAAGATCAAGAACATGGGCCCAGTGTCGTGTCATCGCGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GAGGAGCCGGTTCCCGCAGCTGGAAAAGATCAAGAACATGGGCCCAGTGTCGTGTCATCGCGG 3120

Qy  3121 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCCGCTCCCACATCACTGCCCGCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCCGCTCCCACATCACTGCCCGCT 3180

Qy  3181 GACTACGCCATGCGGCTCATGGAGCAGGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
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Db  3181 GACTACGCCATGCGGCTCATGGAGCAGGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240

Qy  3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTCGTGTCATCGGGGCTCGG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTCGTGTCATCGGGGCTCGG 3300

Qy  3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTTCAGTCGTATGGACAGCACG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTTCAGTCGTATGGACAGCACG 3360

Qy  3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTTCTAGCTGCCAAGGGC 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTTCTAGCTGCCAAGGGC 3420
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Db  1201 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTCAGGGCTGCCGGAGGCCCGG 1320
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Qy  1321 GCCGACCATGCCCACTGCTGTGTGGAGTAGACATGACATGAGTAGGGCCATCTCGCTG 1380
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Qy  1381 GTACGTGAGTGACAGGTGTGAATGTGAACATGCGGTGGCATCCACAGCGGCGCGTG 1440
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Qy  1441 CACTGCGGCGTCCTTGGCTTGCTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1501 CTGGCCAACCACATGAGGAGGCAGGAGGCCGGCTGCCGGCGATCACATCACTCGGGCAACA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CTGGCCAACCACATGAGGAGGCAGGAGGCCGGCTGCCGGCGATCACATCACTCGGGCAACA 1560

Qy  1561 CTGCAGTACTGAACGGGGACTACGAGGTGTGGAGCCAGGCCGTGTGGGCGCAACGCG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 CTGCAGTACTGAACGGGGACTACGAGGTGTGGAGCCAGGCCGTGTGGGCGCAACGCG 1620

Qy  1621 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCTGGGCGCCAGCCAGCAGAAACGGAAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 GAGGAGAAGGCCATGCTGCGCAAGCTGCAGCGGACTCGGCAGCCAACTCCATGGAAGGGCTG 1740

Qy  1741 ATGCCGCGCTGGGGTTCCTGATCGTGTCCCCGGACCAAGGACTCCAAGGGCCTTCCGC 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 ATGCCGCGCTGGGGTTCCTGATCGTGTCCCCGGACCAAGGACTCCAAGGGCCTTCCGC 1800

Qy  1801 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1861 GAGGATGAGGTGAGTTCCTGAGCCGTGCCATGCAGCATTGATCAGCTG 1920
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Db  1981 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTCTGTTGTCTTC 2040

Qy  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCATCTCCACACTCACCCTGATGCTTCGGGATC 2100
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Db  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCATCTCCACACTCACCCTGATGCTTCGGGATC 2100

Qy  2101 TATGCCAGCATCTTTCCTGCTGCTCATCACCGTGATCTGCTGTGTGCTTCCTGT 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TATGCCAGCATCTTTCCTGCTGCTCATCACCGTGATCTGCTGTGTGCTTCCTGT 2160

Qy  2161 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGATTGTCCGCTCACGGGCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGATTGTCCGCTCACGGGCA 2220

Qy  2221 CATAGCACCGCAGTTGGCATCTTTTCCGTGCCTCTGTTGTTTACTTCTGCCATTGCCAAC 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATAGCACCGCAGTTGGCATCTTTTCCGTGTTGTTTACTTCTGCCATTGCCAAC 2280

Qy  2281 ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA 2340
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Qy   3421 TACCAGCTGGAGTGTCGAGGGTGGTCAAGTGAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TACCAGCTGGAGTGTCGAGGGTGGTCAAGTGAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3480

Qy   3481 TTCCTCAATGGGGGCCCAGCAGTTAACAGGGCCCAGCCCACAAATTCAGCTGAAGGGACC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TTCCTCAATGGGGGCCCAGCAGTTAACAGGGCCCAGCCCACAAATTCAGCTGAAGGGACC 3540

Qy   3541 AAGGTGGGCACT 3552
          ||||||||||||
Db   3541 AAGGTGGGCACT 3552
```

RESULT 3
AAX00461
ID   AAX00461 standard; cDNA; 4942 BP.
XX
AC   AAX00461;
XX
DT   21-MAY-1999 (first entry)
XX
DE   Human type VI adenylyl cyclase cDNA.
XX
KW   Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   145..3651
FT   /*tag= a
XX
PN   WO9901547-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998; 98WO-US13594.
XX
PR   01-JUL-1997; 97US-0886550.
PR   01-JUL-1997; 97US-0070904.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Tomlinson JA;
XX
DR   WPI; 1999-106049/09.
DR   P-PSDB; AAW30599.
XX
PT   Newly isolated and purified human type VI adenylyl cyclase (hAC6)
PT   polypeptide - useful for identifying potential therapeutic agents
PT   that modulate hAC6 activity, and for the diagnosis of
PT   hAC6-associated diseases and disorders
XX
PS   Claim 3; Fig 1A-I; 42pp; English.
XX
CC   This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see
CC   AAW30599) that is expressed mainly in the heart and brain. hAC6 has
CC   a similar putative structure to other adenylyl cyclase isoforms
CC   but, like type V, is distinguishable in that it has a larger
CC   N-terminus and a relatively shorter C-terminus as it lacks the C2b
CC   region. hAC6 cDNA was initially isolated from a human heart cDNA
CC   library using an adenylyl cyclase PCR fragment as probe. It was
CC   used to design primers that were used in a PCR-based RACE to obtain
CC   the full-length cDNA sequence. The invention relates to the hAC6
CC   gene, methods for the recombinant production of purified hAC6 and
CC   the proteins made by these methods, antibodies against hAC6,
CC   vectors, probes and host cells (especially HEK-293) transformed by
CC   genes encoding polypeptides having hAC6 activity, along with
CC   diagnostic and therapeutic uses for these various reagents. hAC6
CC   can be used as a tool to screen for agonists and antagonists that
CC   stimulate/inhibit hAC6. Such compounds have therapeutic utility
CC   in treating diseases caused by aberrant activity of this enzyme,
CC   and diseases whose symptoms can be ameliorated by stimulating or
CC   inhibiting the activity of hAC6.
XX
SQ   Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;

Query Match   99.8%; Score 3545.6; DB 20; Length 4942;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3548; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   1 ATGTCATGGTTAGTGCCTCCTGGTCCTAAAGTGACGATGAACGGAAAAACAGCCTGGGGT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTCATGGTTTAGTGCCTCCTCCTGGTCCTAAAGTGACGATGAACGGAAAACAGCCTGGGGT 204

Qy   61 GAACGCAATGGGCAGAAGCGGTTCGCGGCGCCGTGGCACTCGGCGCACTCGGCGCAGTGGCTTCTGCACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205 GAACGCAATGGGCAGAAGCGGTTCGCGGCGCCGTGGCACTCGGCGCACTCGGCGCAGTGGCTTCTGCACG 264

Qy   121 CCCCGCTATATGAGCTGCCTCCGGGATGACAGCTGCAGAGCCACCCAGCCCCACCCTGCGGGGCCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 CCCCGCTATATGAGCTGCCTCCGGGATGACAGCTGCAGAGCCACCCAGCCCCACCCCTGCGGGGCCCC 324

Qy   181 CCTCGGTGCCCCTGGCAGGATGACGGCCTTCATCCGGAGGGGGCGGCCAGGCAAGGGCAAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 CCTCGGTGCCCCTGGCAGGATGACGGCCTTCATCCGGAGGGGGCGGCCAGGCAAGGGCAAG 384

Qy   241 GAGCTGGGGCTCGCGGCAGTGGCCCTGGCTTCGGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 GAGCTGGGGCTCGCGGCAGTGGCCCTGGCTTCGGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 444

Qy   301 GGCGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCATCCTGCTGGCGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGGATCCTGCTGGCGC 504

Qy   361 CGTCTCGGTGCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGCTGGGAGCGGCCTGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 CGTCTCGGTGCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGCTGGGAGCACCTGTAC 564

Qy   421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCTGGGTGGCGGTGCGATGGCGTGCTGGTG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCTGGGTGGCGGTGCGATGGCGTGCTGGTG 624

Qy   481 CTGCTCACAGCGGTGCTGCTGGCTTTCCACGCGCACCCGCCCGCGCCCTCAGCCTGCCTAT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 CTGCTCACAGCGGTGCTGCTGGCTTTCCACGCGCACCCGCCCGCGCCCTCAGCCTGCCTAT 684

Qy   541 GTGGCACTGTTGGCCTTGCCGCGCCGTGCCCCGTTCGTGGGCTCATGGTGGGTGTAACCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 GTGGCACTGTTGGCCTTGCCGCGCCGTGCCCCGTTCGTGGGCTCATGGTGGGTGTAACCGG 744

Qy   601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTACGTCGTGAGTTGCTGCTGGGCATCCTGCG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTACGTCGTGAGTTGCTGCTGGGCATCCTGCG 804

Qy   661 GCAGTGCAGGTCGGGGGCGCTCGCGACAGCACCCGCAGACCCGCCAGCCCCTCGCGGGCCTCGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805 GCAGTGCAGGTCGGGGGCGCTCGCGACAGCACCCGCAGACCCGCCAGCCCCTCGCGGGCCTCGG 864

Qy   721 TGCCCTGGTGTCTTTTGTCTACATCGGCTACACGCGCTCTCCCCATCGCCATGCGGGGCTGCC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865 TGCCCTGGTGTCTTTTGTCTACATCGGCTACACGCGCTCTCCCCATCGCCATGCGGGGCTGCC 924

Qy   781 GTCTTCCAGGGCCTGGGGCCTGCACCTTGCATTTGATCTTCGGCCTGGCAACTTAACCGT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 GTCCTCCAGGGCCTGGGGCCTGCACCTTGCATTTGATCTTCGGCCTGGCAACTTAACCGT 984

Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAAATGTGCTCGTGTTCCTCTGTCACCAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTCGTGTTCCTCTGCACCAAC 1044

Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGGCCTTTCAGGAG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGGCCTTTCAGGAG 1104

Qy   961 ACCCGGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGGAGGCGG 1020
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Qy  1105 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACCCGCGGTTACATCCAGGCCCGGCTTCCACCTGGCAGCATGAGATCGGCAGCAGGAGCGGG 1164

Db  1021 CTGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCATGGACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165 CTGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACACATCAACACA 1224

Qy  1081 AAAAAGAAGACACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 AAAAAGAAGACACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC 1284

Qy  1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGCACATCCCAGTGCACTGCGCAGGAGGCTG 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285 CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGCACATCCCAGTGCACTGCGCAGGAGGCTG 1344

Qy  1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGTGCGCGGAGAATCACTGC 1404

Qy  1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCCGG 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCCCGG 1464

Qy  1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATTCGCGCTG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1465 GCCGACCACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1524

Qy  1381 GTACGTGAGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1525 GTACGTGAGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1584

Qy  1441 CACTGCGGGCGTCCTTGGCTTGCCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1585 CACTGCGGGCGTCCTTGGCTTGCCGGAAATGGCAGTTCGATGTGTGTCCAATGATGTGACC 1644

Qy  1501 CTGGCCACCACATGGCAGCAGGAGGCCGGGCTGGCCGCGATCCACATCACTCGGGCAACA 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1645 CTGGCCAACCACACATGGAGGCAGGAGGCCGGGCTGGCCCGGCTCACATCACTCGGGCAACA 1704

Qy  1561 CTGCAGTACTTGAAACGGGGACTACGAGAGCACTGCGTGTGTGGCCAGGCCAACGCGCG 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1705 CTGCAGTACTTGAAACGGGGACTACGAGAGCACTGCGTGTGTGGCCAGGCCAACGCGCG 1764

Qy  1621 TACCTCAAGGAGCAGCACATTGATGATTCCAGCAAAGACAACCGGGGCCAGCCAGATGCCCTGAAACCCT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1765 TACCTCAAGGAGCAGCACATTGATGATTCCAGCAAAGACAACCGGGGCCAGCCAGATGCCCTGAAACCCT 1824

Qy  1681 GAGGAGGAGGGCCATGCTGGCCAAGCTGCAGCCGGACTCCGGCCAACTCCATGGAAGGGCTG 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1825 GAGGAGGAGGGCCATGCTGGCCAAGCTGCAGCCGGACTCCGGCCAACTCCATGGAAGGGCTG 1884

Qy  1741 ATGCCGCGCTGGGTTCCTGCCTTCTCGCTCACCTTCAGAGAGGACTCCAAGGCCTTCCGC 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1885 ATGCCGCGCTGGGTTCCTGCCTTCTCGCTCACCTTCAACAGAGGATCTCAAGGCCTTCCGC 1944

Qy  1801 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAAACCCT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1945 CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAAACCCT 2004

Qy  1861 GAGGAGGAGGGCTGGATGAGTTCCTGCGCCATCGATGCCGCAGCATTGATCAGCTG 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2005 GAGGAGGAGGGCTGGATGAGTTCCTGCGCCATCGATGCCGCAGCATTGATCAGCTG 2064

Qy  1921 CGGAAGGACCATGTGCGGCCGGTTTCTGCTCACCTTCTCGCTCTCAAGAGAGGATCTTGAGAAGAG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2065 CGGAAGGACCATGTGCGGCCGGTTTCTGCTCACCTTCTCGCTCTCAAGAGAGGATCTTGAGAAGAG 2124

Qy  1981 TACTCCCGAAGGTGGATCCCGCCTTCGGAGCCTACGTTGCCTGTGCCCTGGTCTTC 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2125 TACTCCCGAAGGTGGATCCCGCCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTTC 2184

Qy  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCCACCCTGATGCTGCTGGGATC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCCACCCTGATGCTGCTGGGATC 2244
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Db  2185 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCCACCCTGATGCTGTGGGATC 2244

Qy  2101 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGTCGATCGTGTCGTGTACTCCTGT 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2245 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGTCGATCGTGTCGTGTACTCCTGT 2304

Qy  2161 GGTTCTCTGTTCCCTGGAAGGCCCTGCTGTTCCGGCAGCATTGTCCGCTCACGGGCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2305 GGTTCTCTGTTCCCTGGAAGGCCCTGCTGTTCCGGCAGCATTGTCCGCTCACGGGCA 2364

Qy  2221 CATAGCACCGCAGTTGGCATCTTTTCCGTTGTGTTTACTTCTGCCATTGCCAAC 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2365 CATAGCACCCCAGTTGGCATCTTTCCGTTGTGTTTACTTCTGCCATTGCCAAC 2424

Qy  2281 ATGTTCACCTGTAACCACCACCCCCATACGGAGCTGTGCAGCGTGCCGTGAATTTAACA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2425 ATGTTCACCTGTAACCAACCACCCCCATACGGAGCTGTGCAGCGTGCCGTGAATTTAACA 2484

Qy  2341 CCTGCTGACATCACTGCCTGCCACCTGCGCAGCAGCTCAATTACTCTCTGGGGCCTGATGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2485 CCTGCTGACATCACTGCCTGCCACCTGCGCAGCAGCTCAATTACTCTCTGGGGCCTGGCCACC 2544

Qy  2401 CCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2545 CCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG 2604

Qy  2461 CTGCTGAGTCTTTGGCAGCTGTCAGCTGGCAGGAGGTGGCCCTCAAATATGACCCCGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2605 CTGCTGAGTCTTTGGCAGCTGTCAGCTGGCAGGAGGTGGCCCTCAAATATGACCCCGTG 2664

Qy  2521 ATGATCTTTGTGTTTTGCGGCTCATCTATTGGTGCGCTGTATCGCAGTGGAGTGCGACTGCC 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2665 ATGATCTTTGTGTTTTGCGGCTCATCTATTGGTGCGCTGTATCGCAGTGGAGTGCGACTGCC 2724

Qy  2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCATGGCTTCGTTCTTCCAATGAGACC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2725 ATCTTTGACAACTATGACCTACTGCTTGGCGTCATGGCTTCGTTCTTCCAATGAGACC 2784

Qy  2641 TTTGATGGGCTGGACTGTCCAGCTGGCAGGGAGGTGGCGCCCTCAAATATATGACCCCGTG 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2785 TTTGATGGGCTGGACTGTCCAGCTGTGCAGGGAGGTGGCGCCCTCAAATATATGACCCCGTG 2844

Qy  2701 ATTCTGCTGTGTTTGCGGCTGTATCGCAGTGGAGTGCGACTGCC 2760
         |||||||||||||||||||||||||||||||||||||||||||||
Db  2845 ATTCTGCTGTGTTTGCGGCTGTATCGCAGTGGAGTGCGACTGCC 2904

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAACACAGGGGAGAGATGGGAGGAGCTA 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2905 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAACACAGGGGAGAGATGGGAGGAGCTA 2964

Qy  2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCAAGGACTCCCACTTC 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2965 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACTCCCACTTC 3024

Qy  2881 CTGGCCGGAGCCGGTTCCGGCAGCTGGAATGAGCGCGCGAATGAACTCTACTATCAGTCGTGTGGCTGTT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3025 CTGGCCGGAGCCGGTTCCGGCAGCTGGAATGAGCGCGCGAATGAACTCTACTATCAGTCGTGTGGCTGTT 3084

Qy  2941 ATGTTTGCCTTCCATTGCCAACTTCTCTGAGTTCTCATGTGGAGGCTTGGAGGCAAACAATGAG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3085 ATGTTTGCCTTCCATTGCCAACTTCTCTGAGTTCTCATGTGGAGGCTTGGAGGCAAACAATGAG 3144

Qy  3001 GGTGTCGAGTGTGCTGCTCGCCCCGGTTTCTCGCTCAACAGAGATCATCGCTGCTGACTTTGATGAGATTATCAGC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3145 GGTGTCGAGTGTGCTGCTCGCCCCGGTTTCAACGAGATCATCGCTGCTGACTTTGATGAGATTATCAGC 3204

Qy  3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCGC 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3205 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCGC 3264

Qy  3121 TCAGGGCTGAACGCCAGCAGCCAGCTACGATCAGGTGCGGCGCTGCCCATCACTGCCCTGGCT 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3265 TCAGGGCTGAACGCCAGCAGCCAGCTACGATCAGGTGCGGCGCTGCCCATCACTGCCCTGGCT 3324
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Example 5; Page 122-129; 153pp; English.

PS
XX
CC   The present invention relates to methods and compositions for enhancing
CC   cardiac function in mammalian hearts by inserting transgenes encoding
CC   beta-adrenergic signalling proteins (beta-ASP) which increase
CC   beta-adrenergic responsiveness within the myocardium using in vivo
CC   gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC   receptors (beta-AR), adenylylcyclases (also referred as adenylylcyclase,
CC   adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC   (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC   in mammalian hearts and for treating heart disease, especially
CC   congestive heart failure. The present DNA sequence encodes human
CC   cardiac adenylylcyclase VI (ACVI) isoform which is used for generating
CC   a third beta-ASP transgene, used in the exemplification
CC   of the invention.
XX
SQ   Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match             98.1%;  Score 3484.8;  DB 22;  Length 3549;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 3517;  Conservative    0;  Mismatches   32;  Indels   3;  Gaps   1;

Qy          1 ATGTCATGGTTAGTGCCTCCTGGTCCTAAAGTGATGAACGGAAAACAGCCTGGGGT   60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCATGGTTAGTGCCTCCTGGTCCTAAAGTGATGAACGGAAAACAGCCTGGGGT   60

Qy         61 GAACGCAATGGGCAGAAGCGTTCGGCGGCGGCCGGTGGCTTCTCGCACG  120
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAACGCAATGGGCAGAAGCGTTCGGCGGCGGCCGGTGGCTTCTCGCACG  120

Qy        121 CCCGGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCGCGGGCCCC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCGCGGGCCCC  180

Qy        181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGCCCAGGCAAGGGCAAG  240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGCCCAGGCAAGGGCAAG  240

Qy        241 GAGCTGGGGCTGCGGGCAGTGGCCTTCGGGCTTCGAGGATACCGAGGTGACAACGAGCG  300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTGGGGCTGCGGGCAGTGGCCTTCGGGCTTCGAGGATACCGAGGTGACAACGAGCG  300

Qy        301 GGCGGGACGCGGCTGAGGTGGCGCGCCGACGCGGTGGCGATCCTGCTGGCGC  360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCGGGACGCGGCTGAGGTGGCGCGCCGACGCGGTGGCGATCCTGCTGGCGC  360

Qy        361 CGTCTGTGCAGGTGTTCCAGTGCAAGCAGTTCCGTTCGGCCAAGCTGGAGCGGCCTGTAC  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTTTGGTGCAGGTGTTCCAGTGCAAGCAGTTCCGTTCGGCCAAGCTGGAGCGGCCTGTAC  420

Qy        421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCAGCCTGACGCTGCTGATGGCGGTGCTGTG  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGCGGTACTTTTTCCAGATGAACCAGAGCAGCAGCCTGACGCTGCTGGTGGCGGTGCTGTG  480

Qy        481 CTGCTCACAGCGGTGCTGCTGGCTTTCACGCCGCCACCCGCCCCTCAGCCTGCCTAT  540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAGCGCCACCCGCCCCTCAGCCTGCCTAT  540

Qy        541 GTGGCACTGTTGGCCTGCGCCGGGCTTCGTGGGGCTCATGGTGTGGTGTAACCGG  600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGCACTGTTGGCCTGCGCCGGGCTGTTCGTGGGGCTCATGGTGTGGTGTAACCGG  600

Qy        601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTACGTGGTGCTGGGCATCCTGCGC  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGCGC  660

Qy        661 GCAGTGCAGGTGGGGGGCGCTCGCAGCAGACCCGCCTCTGG  720
              |||||||||||||||||||||||||||||||||||||||||
Db        661 GCAGTGCAGGTGCGGGGGCGCTTCGCAGCAGACCCGCCTCTGG  720

Qy        721 TGCCCTGTGTTCTTTGTCTACATCGCCTACACGCTCTCCCATCCGCATGCGGGCTGCC  780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGCCCTGTGTTCTTTGTATACATCGCCTACACGCTCTCCCATCCGCATGCGGGCTGCC  780
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Qy       3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3325 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3384

Qy       3241 TTCCAGATGAAGAATTGGGCTGCAACATGGGCCCAGTGCTGGCAGGGTCATCGGGGTCGG  3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3385 TTCCAGATGAAGAATTGGGCTGCAACATGGGCCCAGTGCTGGCAGGGTCATCGGGGCTCGG  3444

Qy       3301 AAGCCACCAGTATGACATCTCGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG  3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3445 AAGCCACCAGTATGACATCTCGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG  3504

Qy       3361 GGGGTCCCCGACCGAATCCAGTGACCACGGACCCTGTACCAGGTTCTAGCTGCCAAGGGC  3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3505 GGGGTCCCCGACCGAATCCAGTGACGTGACCACGGACCCTGTACCAGGTTCTAGCTGCCAAGGGC  3564

Qy       3421 TACCAGCTGGAGTGTGCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGCAAGAGAGATGACCACCTAC  3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3565 TACCAGCTGGAGTGTGCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGCAAGAGAGATGACCACCTAC  3624

Qy       3481 TTCCTCAATGGGGGGCCCAGCAGTTAACAGGGCCCAGCCCCACAAATTCAGCTGAAGGGACC  3540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3625 TTCCTCAATGGGGGGCCCCAGCAGTTAACAGGGCCCAGCCCACAAATTCAGCTGAAGGGACC  3684

Qy       3541 AAGGTGGGCACT  3552
              ||||||||||||
Db       3685 AAGGTGGGCATT  3696
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RESULT 4
AAD08563
ID   AAD08563 standard; DNA; 3549 BP.
XX
AC   AAD08563;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human cardiac adenylylcyclase VI (ACVI) isoform #1 DNA.
XX
KW   Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW   myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW   adenylylcyclase; adenylate cyclase; cAMP synthetase;
KW   G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW   cardiac adenylylcyclase VI; ACVI isoform; beta-ASP transgene; ds.
XX
OS   Homo sapiens.
XX
FH            Key             Location/Qualifiers
FT   CDS             1..3504
FT                   /*tag=  a
FT                   /product= "Human cardiac adenylylcyclase VI isoform #1"
FT                   /EC_number= "4.6.1.1"
XX
PN   WO200148164-A2.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US35411.
XX
PR   27-DEC-1999; 99US-0472667..
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Hammond HK, Gao M;
XX
DR   WPI; 2001-418260/44.
DR   P-PSDB; AAE04310.
XX
PT   Novel polynucleotide encoding a modified adenylylcyclase polypeptide
PT   useful for enhancing cardiac function in mammalian hearts, and for
PT   treating heart disease, especially congestive heart failure -
XX
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Qy  781  GTCCTCAGCGGCCTGGGCCTTCTCCACCTTGATCTTGGCCTGGCAACTTAACCGT  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GTCCTCAGCGGCCTGGGCCTTCTCCACCTTGATCTTGGCCTGGCAACTTAACCGT  840

Qy  841  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTTCCTCGCACCAAC  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTTCCTCTGCACCAAC  900

Qy  901  GTCATTGGCATCTGCACACTATCCAGACAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  GTCATTAGCATCTGCACACATATCAGACAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG  960

Qy  961  ACCCGCGGTTACATCCAGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGGAGGAGCGG  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  ACCCGCAGTTACATCCAGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGGAGGAGCGG  1020

Qy 1021  CTGCTGCTGTCGGTATTGCCCAGACAGTTGCCAATGGCCAATGTGCTGTCTCTGCGACCAC  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  CTGCTGCTGTCGGTATTGCCCAGACAGTTGCCAATGGCCAATGTGCTGTCTCTGCGACCAC  1080

Qy 1081  AAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC  1140
         ||||||||||||||           |||||||||||||||||||||||||||||||||||
Db 1081  AAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC  1137

Qy 1141  CTGTTTTGCAGACATTGAGGGCTTCACCAGGCTTACTACTGTGTGCACTGCGCAGGAGCTG  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1138  CTGTTTTGCAGACATTGAGGGCTTCACCAGGCTTACTACTGTGTGCACTGCGCAGGAGCTG  1197

Qy 1201  GTCATGACCCTGAATGAGCTCTTTTGCACAAGCTGGCTGCGGAGAATCACTGC  1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1198  GTCATGACCCTGAATGAGCTCTTTTGCACAAGCTGGCTGCGGAGAATCACTGC  1257

Qy 1261  CTGAGGATCAAGATCTTGGGGGACTTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG  1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1258  CTGAGGATCAAGATCTTGGGGGACTTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG  1317

Qy 1321  GCCGACCCTGACTGCTGTGTGGGAGATGGGGGTAGACACATGATTGAGGCCATCTCGCTG  1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1318  GCCGACCCTGACTGCTGTGTGGGAGATGGGGGTAGACACATGATTGAGGCCATCTCGCTG  1377

Qy 1381  GTACGTGAGGTGACAGGTGACAATGTGAACATGGCAGTTCGATGTGTGTCCAATGATGTGACC  1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1378  GTACGTGAGGTGACAGGTGACAATGTGAACATGGCAGTTCGATGTGTGTCCAATGATGTGACC  1437

Qy 1441  CACTGCCGCGGCGTCCTTGGCTTGGCGGAAATGGCACATTGAGACTTTCCTCATCGTGTCGGGGCAACA  1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1438  CACTGCCGCGGCGTCCTTGGCTTGGCGGAAATGGCACATTGAGACTTTCCTCATCGTGTCGGGGCAACA  1497

Qy 1501  CTGGCCAACCACCACATGGGAGGAGGCGCCGGGCTTGGCCCGATCCACATCACTCCGGGCAACA  1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1498  CTGGCCAACCACCACATGGGAGGAGGCGCCGGGCTTGGCCCGATCCACATCACTCCGGGCAACA  1557

Qy 1561  CTGCAGTACCTGACGGGGACTACGAGGTGGAGCGAGGTGGGCAGGGCGCCTTCGG  1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1558  CTGCAGTACCTGACGGGGACTACGAGGTGGAGCGAGGTGGGCAGGGCGCCTTCGG  1617

Qy 1621  TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCCGCCAGCCAGAAACGGAAA  1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1618  TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCCGCCAGCCAGAAACGGAAA  1677

Qy 1681  GAGGAGAAGGCCATGCTGCTGCCAAGCTCGGCGACTCGGCCAACTCCATGGAAGGGCTG  1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1678  GAGGAGAAGGCCATGCTGCTGCCAAGCTCGGCGACTCGGCCAACTCCATGGAAGGGCTG  1737

Qy 1741  ATGCCGCGCGGCTGGGTTCCTGATCGGTCCTTTCTCCCCGGACCAAGGACTTCAAGGGCCTTCCGG  1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1738  ATGCCGCGATGGGTTCCTGATCGGTCCTTTCTCCCCGGACCAAGGACTTCAAGGGCCTTCCGC  1797

Qy 1801  CAGATGGGCATTGATGATTCCAGCAAAGACACCGGGCACCCGAGATGCCCTGAACCCT  1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1798  CAGATGGGCATTGATGATTCCAGCAAAGACACCGGGCACCCGAGATGCCCTGAACCCT  1857
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Qy 1861  GAGGATGAGGTGATGAGTTCCTGAGCCGTGCCATCGATGCCGAGCATTGATCAGCTG  1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1858  GAGGATGAGGTGATGAGTTCCTGAGCCGTGCCATCGATGCCGAGCATTGATCAGCTG  1917

Qy 1921  CGGAAGGACCATGTGCGCGCGGTTTCTGCTCACCTTCAGAGAGAGGATCTTGAGAAGAAG  1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1918  CGGAAGGACCATGTGCGCGCGGTTTGCTCACCTTCAGAGAGAGGATTTTGAGAAGAAG  1977

Qy 1981  TACTCCCGGAAGGTTGGATCCCCGTTCAGGCGCCAGGCCTTTCAGGAG  2040
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1978  TACTCCCGGAAGGTTGGATCCCCGTTCAGGCGCCAGGCCTTTCAGGAG  2037

Qy 2041  TGCTTCATCTGCTTCATCTTCTCATCTTCCCACACTCCACCTCTTTCCACCCTGATGCTTCGGGATC  2100
         ||||||||||||||||||||||            |||||||||||||||||||||||||||
Db 2038  TGCTTCATCTGCTTCATCTTCTCATCTTCTAATTTCCCACACTCCACCCTGATGCTTCGGGATT  2097

Qy 2101  TATGCCAGCATCTTCCTGCTGCTGTAATCACCGTGCTGATCTGTGTCTGTGTACTTCCTGT  2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2098  TATGCCAGCATCTTCCTGCTGCTGTAATCACCGTGCTGATCTGTGTCTGTGTACTTCCTGT  2157

Qy 2161  GGTTCTTCTGTTCCCTAAGGCCCTGCAACCTCGTCCCGCAGCATTGTCCCGCTCACGGGGCA  2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2158  GGTTCTTCTGTTCCCTAAGGCCCTGCAACCTCGTCCCGCAGCATTGTCCCGCTCACGGGGCA  2217

Qy 2221  CATAGCACCCAGTTGGCATCTTTTCCGTCCTGTGTTTACTTCTGCCATTGCCAAC  2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2218  CATAGCACCCAGTTGGCATCTTTTCCGTCCTGTGTTTACTTCTGCCATTGCCAAC  2277

Qy 2281  ATGTTCACCTGTAACCATCACCACCCCATACCGAGCTGTGCAGCCCGATGCTGAATTTAACA  2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2278  ATGTTCACCTGTAACCATCACCACCCCATACCGAGCTGTGCAGCCCGATGCTGAATTTAACA  2337

Qy 2341  CCTGCTGACATCACTGCCTCTGCTTCTTCCTGCACATCAGCAGCAGCTCAATTACTCTCTGGATGCT  2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2338  CCTGCTGACATCACTGCCTCTGCTTCTTCCTGCACATCAGCAGCAGCTCAATTACTCTCTGGATGCT  2397

Qy 2401  CCCTGTGTGAGGGCACCATGCCAGCTCTTCCTGACTACTTCATCGTCGGAACATG  2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2398  CCCTGTGTGAGGGCACCATGCCAGCTCTTCCTGAGGTCTCATCGTCGGAACATG  2457

Qy 2461  CTGCTGAGTCTCTTGGCCAGCTCGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2458  CTGCTGAGTCTCTTGGCCAGCTCGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2517

Qy 2521  ATGATCTTTGTCTTGGGGTCATCTATTTGGTGCGTCCCCAGCCACC  2580
         |||||||||||||||||||||||||||||||||||||||||||||
Db 2518  ATGATCTTTGTCTTGTGTCTTGGGGTCATCTATTTGGTGCGTCCCCAGCCGCC  2577

Qy 2581  ATCTTTGACAACTATGACCTACTGCTTGGCGTTCATGGCCTTGGCTTCTTCCAATGAGACC  2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2578  ATCTTTGACAACTATGACCTACTGCTTGGCGTTCATGGCCTTGGCTTCTTCCAATGAGACC  2637

Qy 2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGGTGGCCCTCAAATATATGACCCCGTG  2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2638  TTTGATGGGCTGGACTGTCCAGCTGCAGGGTGGCCCTCAAATATATGACCCCGTG  2697

Qy 2701  ATTCTGCGTGGTGTTGCGCTGGCGGCTGGCGTGTATCTCGCAGGTGGACTGCGACTGCC  2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2698  ATTCTGCGTGGTGTTGCGCTGGCGGCTGGCGTGTATCTCGCAGGTGGAATCGACTGCC  2757

Qy 2761  CGCCTAGACTTCCTCTGGAAACTACAGGGAGAACAGGAGATGGAGGAGCTA  2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2758  CGCCTAAACTTCCTCTGGAAACTACAGGGAGAACAGGAGGAAAAAGAGGAGGAGCTA  2817

Qy 2821  CAGGCATCAAGCCGAGGCCGCTGTCGCATAACATTCGCCCAAGGACGTGGCGGGCCCACTTC  2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2818  CAGGCATACAACCCGAGGCCGCTGTCGCATATACATTCGCCCAAGGACGTGGCGGGCCCACTTC  2877

Qy 2881  CTGGCCCGGAGCGCCCAATGAACTTCGCTGAGTTCTATGTGGAGGCAACAATGAG  2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2878  CTGGCCCGGAGCGCCCAATGAACTTCTACTATCAGTCGTGTGAGTTGTGTGGCTGTT  2937

Qy 2941  ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCAACAATGAG  3000
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PR   27-DEC-1999;   99US-0472667.
XX
PA   (HAMM/) HAMMOND H K.
PA   (INSE/) INSEL P A.
PA   (PING/) PING P.
PA   (POST/) POST S R.
PA   (GAOM) GAO M.
XX
PI   Hammond HK, Insel PA,  Ping P,  Post SR,  Gao M;
XX
DR   WPI; 2002-690626/74.
DR   P-PSDB; ABG32868.
XX
PT   Enhancing cardiac function in a mammal for treating heart disease such
PT   as congestive heart failure, by delivering to the heart of the mammal a
PT   vector comprising a gene encoding a beta-adrenergic signalling protein
PT   .
XX
PS   Claim 75; Page 37-38; 69pp; English.
XX
CC   The invention relates to enhancing cardiac function in a mammal,
CC   involves delivering a vector to the heart of the mammal, where the
CC   vector comprises a gene encoding a beta-adrenergic signalling protein
CC   (beta-ASP) e.g. adenylylcyclase isoform 6 (AC-VI) operably linked to a
CC   promoter. Generating a recombinant replication-defective viral particle
CC   involves introducing first and second plasmids into a replication-
CC   permissive mammalian cell expressing one or more adenovirus genes
CC   conferring replication competence, where the first plasmid comprises a
CC   gene encoding a beta-ASP operably linked to a promoter and further
CC   comprises a replication-defective human adenovirus genome, and the second
CC   plasmid comprises a replication-proficient human adenovirus genome and
CC   further comprises an additional polynucleotide sequence making the second
CC   plasmid too large to be encapsidated in an adenovirus particle, where
CC   rescue recombination takes place between the first plasmid and the second
CC   plasmid to generate a recombinant adenoviral genome comprising the gene
CC   encoding a beta-ASP but lacking one or more adenoviral replication genes,
CC   where the recombinant genome is sufficiently small to be encapsidated in
CC   an adenovirus particle, identifying successful recombinant viral vectors
CC   in cell culture, and propagating a resulting recombinant viral particle
CC   in replication-permissive mammalian cells expressing the missing
CC   adenoviral replication genes to generate a recombinant replication-
CC   defective viral particle. The method is useful for enhancing cardiac
CC   function in a mammal, preferably human and is specifically useful for
CC   treating heart diseases such as congestive heart failure (CHF).
CC   The present sequence is a cDNA encoding human Adenylylcyclase
CC   isoform 6, AC-VI, a beta-ASP, used in the method of the invention.
XX
SQ   Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match             98.1%;  Score 3484.8;  DB 24;  Length 3549;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 3517;  Conservative    0;  Mismatches   32;  Indels    3;  Gaps    1;

Qy          1 ATGTCATGGTTTAGTGGCTGCCTTCCCTAAAGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCATGGTTTAGTGGCTGCCTTCCCTAAAGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT  60

Qy         61 GAACGGCAATGGGCAGCAGAAGCGTTCGGCGCCGTCGCCGTCGGCCGCACTCGGGCGGCTTCTCGCACG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAACGGCAATGGGCAGCAGAAGCGTTCGGCGCCGTCGCCGTCGGCCGCACTCGGGCGGCTTCTCGCACG 120

Qy        121 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCCCAGCCACCCCTGCGGGCCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCCCAGCCACCCCTGCGGGCCCC 180

Qy        181 CCTCGGTGCCCCTGCCCAGGATGACGGCCTTCATCCGGAGGGGCCCAGGCAAGGGCAAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTCGGTGCCCCTGCCCAGGATGACGGCCTTCATCCGGAGGGGCCCAGGCAAGGGCAAG 240

Qy        241 GAGCTGGGGCTGCGCGGCAGTGGCCCTGGCCTTGGGGCTTCGGCTTCATCCGGAGGATACCGAGGTGACAACGACGCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTGGGGCTGCGCGGCAGTGGCCCTGGCCTTGGGGCTTCGGCTTCATCCGGAGGATACCGAGGTGACAACGACGCAG 300
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Db       2938 ATGTTTGCCTCCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCGCAAACAATGAG 2997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       3001 GGTGTCGAGTCGCTGCCGCGCTGCCGGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2998 GGTGCCGAGTCGCTGCCGCGCTGCCGGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057

Qy       3061 GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACCATGGCTGCC 3120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3058 GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACCATGGCTGCC 3117

Qy       3121 TCAGGGCTGAACGCCAGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3118 TCAGGGCTGAACGCCAGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3177

Qy       3181 GACTACGCCATGGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3178 GACTACGCCATGGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3237

Qy       3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGCGGCTCGG 3300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGCGGCTCGG 3297

Qy       3301 AAGCCACCAGTATGACATCTCGGGGAACACAGTGAATTGTCTCTAGTCGTATGGACAGCACG 3360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3298 AAGCCACCAGTATGACATCTCGGGGAACACAGTGAATTGTCTCTAGTCGTATGGACAGCACG 3357

Qy       3361 GGGGTCCCCGACCGAATCCAGGTGACCACCGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3358 GGGGTCCCCGACCGAATCCAGGTGACCACCGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3417

Qy       3421 TACCAGCTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTAC 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3418 TACCAGCTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTAC 3477

Qy       3481 TTCCTCAATGGGGGCCCCAGCAGTAACAGGGCCCACAAATTCAGCTGAAGGGACC 3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3478 TTCCTCAATGGGGGCCCCAGCAGTAACAGGGCCCACAAATTCAGCTGAAGGGACC 3537

Qy       3541 AAGGTGGGCACT 3552
              ||||||||||||
Db       3538 AAGGTGGGCACT 3549
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RESULT 5
ABS54133
ID   ABS54133 standard; cDNA; 3549 BP.
XX
AC   ABS54133;
XX
DT   20-NOV-2002 (first entry)
XX
DE   Human cDNA encoding Adenylylcyclase isoform 6, AC-VI.
XX
KW   Human; ss; gene; adenylylcyclase isoform 6; AC-VI; CHF; gene therapy;
KW   beta-adrenergic signalling protein; congestive heart failure; cardiant;
KW   cardiac function; adenovirus vector; transgenic; gene therapy;
KW   beta-adrenergic signalling protein; beta-ASP; heart disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3504
FT                   /*tag= a
FT                   /EC_number= "4.6.1.1"
FT                   /product= "Adenylylcyclase isoform 6"
XX
PN   US2002103147-A1.
XX
PD   01-AUG-2002.
XX
PF   26-DEC-2000; 2000US-0750240.
XX
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DNA sequence alignment (Qy / Db) with position numbering from 301 through 2520.

RESULT 6
AAD08568
ID   AAD08568 standard; cDNA; 3582 BP.
XX
AC   AAD08568;
XX
DT   04-SEP-2001 (first entry)
XX
DE   Human modified cardiac adenylcyclase VI (ACVI) isoform cDNA.
XX
KW   Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW   myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW   adenylylcyclase; adenylate cyclase; cAMP synthetase;
KW   G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW   cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Location/Qualifiers
FT   Key
FT   CDS   22..3525
FT   /*tag= a
FT   /product= "Human modified cardiac ACVI isoform"
XX
PN   WO20148164-A2.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US35411.
XX
PR   27-DEC-1999;   99US-0472667.
XX
PA   (REGC) UNIV CALIFORNIA.
XX
PI   Hammond HK, Gao M;
XX
DR   WPI; 2001-418260/44.
DR   P-PSDB; AAE04312.
XX
PT   Novel polynucleotide encoding a modified adenylylcyclase polypeptide
PT   useful for enhancing cardiac function in mammalian hearts, and for
PT   treating heart disease, especially congestive heart failure -
XX
PS   Claim 4; Page 143-150; 153pp; English.
XX
CC   The present invention relates to methods and compositions for enhancing
CC   cardiac function in mammalian hearts by inserting transgenes encoding
CC   beta-adrenergic signalling proteins (beta-ASP) which increase
CC   beta-adrenergic responsiveness within the myocardium using in vivo
CC   gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC   receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase,
CC   adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC   (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC   in mammalian hearts and for treating heart disease, especially
CC   congestive heart failure. The present cDNA sequence encodes human
CC   modified cardiac adenylcyclase VI (ACVI) isoform which is used for
CC   generating a beta-ASP transgene, used in the exemplification of the
CC   invention.
XX
SQ   Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match   96.9%; Score 3443.2; DB 22; Length 3582;
Best Local Similarity   98.3%; Pred. No. 0;
Matches 3491; Conservative   0; Mismatches   58; Indels   3; Gaps   1;

Qy   1 ATGTCATGGTTTAGTGGCCTCCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 ATGTCATGGTTTAGTGGCCTCCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 81

Qy   61 GAACGGCAATGGCAGAAGCGTTCGCGCGCCGTGCGCGCCCTGGGCACTCGGCGCTTCTCACG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAACGGCAATGGCAGAAGCGTTCGCGCGCCGTGCGCGCCCTGGGCACTCGGCGCTTCTCACG

Db 82 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCACGGAGGTGGCTTCTGCGACG 141
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCACCCAGCCCCACCCCTGCGCGCCCC 180
Db 142 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCGAGAGCACCCAGCCCCACCCCTGCGCGGCCCC 201

Qy 181 CCTCGGTGCCCCTGCCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
Db 202 CCTCCGGTGCCCTGCCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 261

Qy 241 GAGCTGGGGGTGCGGGGCAGTGGCTGGCCCGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
Db 262 GAGCTGGGGGTGCGGGGCAGTGGCTGGCCCGGCTTCGAGGATACCGAGGTGACAACGACAGCG 321

Qy 301 GGCGGGACGCGCTGAGGTGGCGCCCGAGCGCCGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360
Db 322 GGCGGGACGCGCTGAGGTGGCGCCCGAGCGCCGTGCCCAGGAGTGGGCATCCACAGCGGCGCGTG 381

Qy 361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGTTCCGGCCAAGCTGGAGCGCCGTAC 420
Db 382 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGTTCCGGCCAAGCTGGAGCGCCGTAC 441

Qy 421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCTCCATGTGGGTGCGGTGCTGGTG 480
Db 442 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCTCCATGTGGGTGCGGTGCTGGTG 501

Qy 481 CTGCTCACAGCGGTGCTGTGGCTTTCCACGCCCGCACCGCCCTCAGCCTGCCTAT 540
Db 502 CTGCTCACAGCGGTGCTGTGGCTTTCCACGCCCGCACCGCCCTCAGCCTGCCTAT 561

Qy 541 GTGGCACTGTTGGCCGTGTGCCGCGCCCGTTCGTGGGGCTCATGTGGTGTGTAACCGG 600
Db 562 GTGGCACTGTTGGCCGTGTGCCGCGCCCGTTCGTGGGGCTCATGTGGTGTGTAACCGG 621

Qy 601 CATAGCTTCCGGCCAGGAACTCCATGTGGGTTACGTGGTGCTGGGCATCCTGGCG 660
Db 622 CATAGCTTCCGGCCAGGAACTCCATGTGGGTTACGTGGTGCTGGGCATCCTGGCG 681

Qy 661 GCAGTGCAGGTCGGGGGCGCTCTGCGCAGCAGACCCGGCACCCGCGAGCCCCGTCTGG 720
Db 682 GCAGTGCAGGTCGGGGGCGCTCTGCGCAGCAGACCCGGCACCCGCGAGCCCCGTCTGG 741

Qy 721 TGCCCTGTGTTCTTGTTCTTTGTCTACATCGCCTCACGCTCTCCCCATCGGCGGCTGCC 780
Db 742 TGCCCCTGTGTTCTTGTTCTTTGTCTACATCGCCTCACGCTCTCCCCATCGGCGGCTGCC 801

Qy 781 GTCTTCAGCGGCCCTGGGCCTTCCACCTTGCATTGATCTTGGCCTGGCAACTTAACCGT 840
Db 802 GTCTTCAGCGGCCTGGGCCTTCCACCTTGCATTGATCTTGGCCTGGCAACTTAACCGT 861

Qy 841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCGCCGGTTTCGTGTTCCTCTGCACCAAC 900
Db 862 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCGCCGGTTTCGTGTTCCTCTGCACCAAC 921

Qy 901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
Db 922 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 981

Qy 961 ACCCGGCGTTACATCCAGGCCCGGCTCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
Db 982 ACCCGGCGTTACATCCAGGCCCGGCTCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1041

Qy 1021 CTGCTGCTTCGGTATTGCCCCGAGCAGTGTGCCATGGAGAATGAAAGAGACATCAAACA 1080
Db 1042 CTGCTGCTGTCGGTATTGCCCCGAGCACGTTGCCATGGAGAATGAAAGAGACATCAAACA 1101

Qy 1081 AAAAAGAAGACAGATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC 1140
Db 1102 AAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTTCAGCATC 1161

Qy 1141 CTGTTTGCAGACATTGAGGGCTTCACCCAGTCCATCCCAGTGCACTGCCGCAGGAGCTG 1200
Db 1162 CTGTTTGCAGACATTGAGGGCATCCTTTCCACCCAGTCCATCCCAGTGCACTGCCGCAGGAGCTG 1221

Qy 1201 GTCATGACCCTGAATGAGCTCTTCGCCCGGTTGACAAGCTGGCGTGCGAGAATCACTGC 1260
Db 1222 GTCATGACCTTGAATGAGCTCTTTGCCCGGTTGACAAGCTGGCTGCGGAGAATCACTGT 1281

Qy 1261 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCAGGGGTAGCATGATTGAGGCCATCTCGCTG 1320
Db 1282 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCGCGTGTCAGGGGTAGACATGATTGAGGCCATCTCGCTG 1341

Qy 1321 GCCGACCATGCCCACTCGTCTGTGTCGGAGATGGGGTAGACATGGGGTGAACATGGCGTGCATCCACAGCGGCGCGTG 1380
Db 1342 GCAGATCACGCCCACTCGTCTGTGTCGTGTCGGAGATGGGGTAGACATGGGGTGAACATGGCGTGCATCCACAGCGGCGCGTG 1401

Qy 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGGCGGTGCGTGGGCATCCACAGCGGCGCGTG 1440
Db 1402 GTGCGTGAGGTAACAGGTGTAACGTGAACATGGCATCCACAGCGGCGACGTGTG 1461

Qy 1441 CACTGCGGCGTCCTTGGCTTGCGGCGAAATGCAGTTCGATGTGTGTCCAATGATGTGACC 1500
Db 1462 CATTGCGGGGTCCTTGGCCTACGGGAAATGCAGTTTGATGTCTGGTCAAACGATGTGACC 1521

Qy 1501 CTGGCCAACCACATGGAGGCAGGAGCCGGGCTGGCCGCATCCACATCACTCGGCGCAACA 1560
Db 1522 CTGGCTAACCATGGAGGCCGGGGGC---GGCCGGCATCCACATCACTCACTCGGCGTACA 1578

Qy 1561 CTGCAGTACCTGAACGCGGGGACTAGAGGTGGAGCGTGGTGGCGAGCGCAACGCG 1620
Db 1579 CTGCAGTACTTGAACGCGGGGACTATGCAGGTGGAGCGTGGTGGCGAGCGCAATGCG 1638

Qy 1621 TACCTTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCGCCAGAAACGGAAA 1680
Db 1639 TACCTTCAAGGAGCAGCAGTGCATTGAGACCTTCCTCATACTTGGCGCGCCAGCCAAAAACGGAAA 1698

Qy 1681 GAGGAGAAGGCCATGCCAAGCTCGGCGGCCAACTCGGCGGACTCGGCGACTCGGAAGGGGCTG 1740
Db 1699 GAGGAGAAAGCCATGCCAAGCTCGGCGGACTCGGCGGACACGGGCCAACTCCATGGAGGACTG 1758

Qy 1741 ATGCCGCGCTGGGTTCCTGCCTTCTCCCGGACCAAGGACTTCCGGCCTTCCGGC 1800
Db 1759 ATGCCCGCGCTGGGTTCCTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCCGC 1818

Qy 1801 CAGATGGGCATTGATGATTCCAGACAAAGACAACCGGGCACCCGGAGATGCCCTGAACCCT 1860
Db 1819 CAGATGGGCATTGATGATTCAGCAAAAGACAACCGGGGTGCCCAAGATGCTCTGAACCCT 1878

Qy 1861 GAGGATGAGGTGGATGAGTTCCTGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 1920
Db 1879 GAAGATGAGGTGGATGAGTTCCTGGGCCGCCAGCCATCGATGCCCGCAGCATTGATCAGCTG 1938

Qy 1921 CGGAAGGACCATGTGCGCCGGTTTCGCTCACCTTCCAGAGAGGATCTTGAGAAGAAG 1980
Db 1939 CGGAAGGACCATGTGCGCCGGTTTCGCTCACCTTCCAGAGAGGAGATCTTGAGAAGAAG 1998

Qy 1981 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTCACGTTGCCTGTGCCCTGTTGGTCTTC 2040
Db 1999 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTCACGTTGCCTGTGCCCTGTTGGTCTTC 2058

Qy 2041 TGCTTCATCTGCTTCATCCAGCTTCTGCTCGTCTAATCACCGTGCTGTCATCCGTGCTGTCCTGT 2100
Db 2059 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCGATGCTTGGGATC 2118

Qy 2101 TATGCCAGCATCTTCCTGCTGCTCTAATCACCGGTGCTGTGTCTGTGTACTTCCTGT 2160
Db 2119 TATGCCAGCATCTTCCTGCTGCTCTAATCACCGTGCTGTGTCTGTGTACTTCCTGT 2178

Qy 2161 GGTTCTCTGTCTGCTTCCCTAAGGCCCTGCAACGTGTCCCGCCATTGTCCGCTCACGGGGCA 2220
Db 2179 GGTTCTCTGTCTGCTTCCCTAAGGCCCTGCAACGTCTGTCCCGCCAGCATTGTCCGCTCACGGGCA 2238

Qy 2221 CATAGCACCCGCAGTTGGCATCTTTTCGTCCTGCGCACCGGGTTGTGTTACTTCTGCCAAC 2280
Db 2239 CATAGCACCCGCAGTTGGCATCTTTTCCGTCCTGCGCACCGGGTTGTGTTACTTCTGCCAAC 2298

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Db  3379 GGGGTCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCCAAGGGC 3438
         |||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  3421 TACCAGCTGGAGTGTCGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTAC 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3439 TACCAGCTGGAGTGTCGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACCTAC 3498

Qy  3481 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3499 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3558

Qy  3541 AAGGTGGGCACT 3552
         ||||||||||||
Db  3559 AAGGTGGGCACT 3570
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RESULT 7
ABS54138
ID   ABS54138 standard; cDNA; 3582 BP.
XX
AC   ABS54138;
XX
DT   20-NOV-2002 (first entry)
XX
DE   Chimaeric cDNA encoding Adenylylcyclase isoform 6, AC-VI.
XX
KW   Human; ss; gene; adenylylcyclase isoform 6; AC-VI; CHF; gene therapy;
KW   beta-adrenergic signalling protein; congestive heart failure; cardiant;
KW   cardiac function; adenovirus vector; transgenic; gene therapy; mouse;
KW   beta-adrenergic signalling protein; beta-ASP; heart disease.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
XX
FH   Key   Location/Qualifiers
FT   CDS   22..3525
FT   /*tag= a
FT   /EC_number= "4.6.1.1"
FT   /product= "Chimaeric Adenylylcyclase isoform 6"
XX
PN   US2002103147-A1.
XX
PD   01-AUG-2002.
XX
PF   26-DEC-2000; 2000US-0750240.
XX
PR   27-DEC-1999; 99US-0472667.
XX
PA   (HAMM/) HAMMOND H K.
PA   (INSE/) INSEL P A.
PA   (PING/) PING P.
PA   (POST/) POST S R.
PA   (GAOM/) GAO M.
XX
PI   Hammond HK, Insel PA, Ping P, Post SR, Gao M;
XX
DR   WPI; 2002-690626/74.
DR   P-PSDB; ABG32870.
XX
PT   Enhancing cardiac function in a mammal for treating heart disease such
PT   as congestive heart failure, by delivering to the heart of the mammal a
PT   vector comprising a gene encoding a beta-adrenergic signalling protein
PT   -
XX
PS   Claim 16; Page 47-48; 69pp; English.
XX
CC   The invention relates to enhancing cardiac function in a mammal,
CC   involves delivering a vector to the heart of the mammal, where the
CC   vector comprises a gene encoding a beta-adrenergic signalling protein
CC   (beta-ASP) e.g. adenylylcyclase isoform 6 (AC-VI) operably linked to a
CC   promoter. Generating a recombinant replication-defective viral particle
CC   involves introducing first and second plasmid into a replication-
CC   permissive mammalian cell expressing one or more adenovirus genes

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Qy  2281 ATGTTCACCTGTAACCACACCCCCATACGGAGCCGTGTGCAGCCGGATGCTGAATTTAACA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2299 ATGTTCACCTGTAACCACACCCCCATACGGAGCCGTGTGCAGCCGGATGCTGAATTTAACA 2358

Qy  2341 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2359 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT 2418

Qy  2401 CCCCTGTGTGAGGGGCACCATGCCCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2419 CCCCTGTGTGAGGGGCACCATGCCCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATG 2478

Qy  2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2479 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2538

Qy  2521 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGTGCTGCTTCTGCTGGGTCCCCAGCCACC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2539 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGTGCTGCTTCTGCTGGGTCCCCAGCCACC 2598

Qy  2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2599 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2658

Qy  2641 TTTGATGGGCTGGACTGTCCAGCTGACGTGCCCGAGGAGGTGGCCCTCAAATATGACCCCTGTG 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2659 TTTGATGGGCTGGACTGTCCAGCTGACGTGCCCGAGGAGGTGGCCCTCAAATATGACCCCTGTG 2718

Qy  2701 ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2719 ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC 2778

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACACAGGGAGGAGATGGAGGAGGAGCTA 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2779 CGCCTAGACTTCCTCTGGAAACTACAGGCAACACAGGGAGGAGATGGAGGAGGAGCTA 2838

Qy  2821 CAGGCATACAACCGGAGGCGTGCTCATAACATTCTGCCCAAGGACGTGGCGCGCCCACTTC 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2839 CAGGCATACAACCGGAGGCGTGCTCATAACATTCTGCCCAAGGACGTGGCGCGCCCACTTC 2898

Qy  2881 CTGGCCCCGGAGCGCGCGCAATGATGAAGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2899 CTGGCCCCGGAGCGCGCGCAATGATGAAGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2958

Qy  2941 ATGTTTGCCTCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCAAACAATGAG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2959 ATGTTTGCCTCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCAAACAATGAG 3018

Qy  3001 GGTGTCGAGTGCCTGCGCGGGCTGCTCAACGAGATCATCCGACTTTGATGAGATTATCAGC 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3019 GGTGTCGAGTGCCTGCGCGGGCTGCTCAACGAGATCATCCGACTTTGATGAGATTATCAGC 3078

Qy  3061 GAGGAGCGGGTTCCGGGCAGCTGGCAGCTGAAAAGATCAAGACGATTGGTAGCACCATGGCTGCC 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3079 GAGGAGCGGGTTCCGGGCAGCTGGCAGCTGAAAAGATCAAGACGATTGGTAGCACCATGGCTGCC 3138

Qy  3121 TCAGGGCTGAACGCGGTGGGCGGTGGGGCTCCCCACATCACTGCCCTGGCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3139 TCAGGGCTGAACGCGGTGGGCGGTGGGGCTCCCCACATCACTGCCCTGGCT 3198

Qy  3181 GACTACGCCATGCGGCTCATGGAGCAGAGTGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3199 GACTACGCCATGCGGCTCATGGAGCAGAGTGAAGCACATCAATGAGCACTCCTTCAACAAT 3258

Qy  3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTGTCAGGTGTCATCGGGGCTCGG 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3259 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTGTCAGGTGTCATCGGGGCTCGG 3318

Qy  3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTCTCGTAGTCGTATGGACAGCACG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3319 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTCTCGTAGTCGTATGGACAGCACG 3378

Qy  3361 GGGGTCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCCAAGGGC 3420
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CC   conferring replication competence, where the first plasmid comprises a
CC   gene encoding a beta-ASP operably linked to a promoter and further
CC   comprises a replication-defective human adenovirus genome, and the second
CC   plasmid comprises a replication-proficient human adenovirus genome and
CC   further comprises an additional polynucleotide sequence making the second
CC   plasmid too large to be encapsidated in an adenovirus particle, where
CC   rescue recombination takes place between the first plasmid and the second
CC   plasmid to generate a recombinant adenoviral genome comprising the gene
CC   encoding a beta-ASP but lacking one or more adenoviral replication genes,
CC   where the recombinant genome is sufficiently small to be encapsidated in
CC   an adenovirus particle, identifying successful recombinant viral vectors
CC   in cell culture, and propagating a reuslting recombinant viral particle
CC   in replication-permissive mammalian cells expressing the missing
CC   adenoviral replication genes to generate a recombinant replication-
CC   defective viral particle. The method is useful for enhancing cardiac
CC   function in a mammal, preferably human and is specifically useful for
CC   treating heart diseases such as congestive heart failure (CHF).
CC   The present sequence is a chimaeric cDNA encoding human/mouse
CC   Adenylylcyclase isoform 6, AC-VI, a beta-ASP, used in the method of the
CC   invention.
XX
SQ   Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match             96.9%;  Score 3443.2;  DB 24;  Length 3582;
Best Local Similarity   98.3%;  Pred. No. 0;
Matches  3491;  Conservative   0;  Mismatches  58;  Indels   3;  Gaps   1;

Qy        1 ATGTCATGGTTTAGTGGCCTCCTGGTCCTAAAGTGGATGAACCGAAAACAGCCTGGGGT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       22 ATGTCATGGTTTAGTGGCCTCCTGGTCCTAAAGTGGATGAACCGAAAACAGCCTGGGGT   81

Qy       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTTGGCCACTCGGGCGGCCTTCTGCACG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       82 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTTGGCCACTCGGGCGGCCTTCTGCACG  141

Qy      121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCCACCCGGGCGGGCCCC          180
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      142 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCCACCCGGGCGGGCCCC          201

Qy      181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCAGGGGCAAG       240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      202 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCAGGGGCAAG       261

Qy      241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      262 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG  321

Qy      301 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCGCCCCGACGCGGTGCGCCCCGAC     360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      322 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCGCCCCGACGCGGTGCGCCCCGAC     381

Qy      361 CGTCTGGTGCAGTGTTCCAGTGCGAAGCAGTTCCGTTCGCGTTCGAGGCGCCTGTAC    420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 CGTCTGGTGCAGTGTTCCAGTGCGAAGCAGTTCCGTTCGCGTTCGAGGCGCCTGTAC    441

Qy      421 CAGCGGTACTTCTTCCAGATGAACCAGAGACAGCCAGCTTGATGGCGGTGCTGGTG      480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      442 CAGCGGTACTTCTTCCAGATGAACCAGAGACAGCCAGCTTGATGGCGGTGCTGGTG      501

Qy      481 CTGCTCACGACGTTGCTGCTGGCTTTCCACGCCGCACCCGGGCGCCCCAGCGCCTAT     540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      502 CTGCTCACGACGTTGCTGCTGGCTTTCCACGCCGCACCCGGGCGCCCCAGCGCCTAT     561

Qy      541 GTGGCACTGTTGGCCGCCGTGTGCCGGCCCCGTGTTCCGTCGGGCTCATGGGGCTGTGTAACCGG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      562 GTGGCACTGTTGGCCGCCGTGTGCCGGCCCCGTGTTCCGTCGGGCTCATGGGGCTGTGTAACCGG  621

Qy      601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTTACGTGCGGTGGGCATCCTGCGG       660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      622 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTTACGTGCGGTGGGCATCCTGCGG       681

Qy      661 GCAGTGCAGGTCGGGGGGCGGCTCTCGCAGCAGAGACCCGGCAGCCCTCGCGGCCTTCGG  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      682 GCAGTGCAGGTCGGGGGGCGGCTCTCGCAGCAGAGACCCGGCAGCCCTCGCGGCCTTCGG  741

Qy      721 TGCCCGTGTTCTTTGTCACATGCCTACACGCTCCTCCCCATCCGCATGCGGCGGCTGCC   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      742 TGCCCGTGTTCTTTGTCACATGCCTACACGCTCCTCCCCATCCGCATGCGGCGGCTGCC   801

Qy      781 GTCCTCAGCGGCCTCGGGCCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      802 GTCTTCAGCGGCCTCGGGCCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT   861

Qy      841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      862 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC  921

Qy      901 GTCATTGGCATCTGCACACTATCCAGCAGAGTGTCTCAGCCGCCAGGCCTTTCAGGAG    960
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      922 GTCATTGGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCCGCCAGGCCTTTCAGGAG  981

Qy      961 ACCCGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      982 ACCCGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1041

Qy     1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGACGATGAAAGAAGACATCAACACA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1042 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGACGATGAAAGAAGACATCAACACA 1101

Qy     1081 AAAAAAGAGACATGATGTTCCACAAGATCTACATACACAGAAGCATGACAATGTCAGCATC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1102 AAAAAAGAGACATGATGTTCCACAAGATCTACATACACAGAAGCATGACAATGTCAGCATC 1161

Qy     1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGCATCCCAGTGCGCCAGGAGCTG       1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1162 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGCATCCCAGTGCGCCAGGAGCTG       1221

Qy     1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1222 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGT 1281

Qy     1261 CTGAGGATCAAGATCTTGGGGACTGTTACTACGTCTGTGTGCTGCGTGTCAGGCCCCGG   1320
            ||||||||||||||||| |||||||||||||| |||||||||||||||||||| ||||||
Db     1282 CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGCGTGTGTGCTGCGTGTCAGGGCCCGG 1341

Qy     1321 GCCGACCATGCCACTGCTTGCTGTGTGGAGATGGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
            || | ||||||| ||||||||||||||||||||||||||||||| ||||||||||||||
Db     1342 GCAGATCACGCCCACTGCTGTGTGGAGATGGGGGGTAGACATGATCGAGGCCATCTCGCTG 1401

Qy     1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCATCCACAGCGGCGCGTGTG 1440
            || |||||||| |||||||| ||| |||||||||||| ||||||||||||||||| |||||
Db     1402 GTGCGTGAGGTAACAGGTGTAACGGTGTGAACGTGAACATGCGTGGCATCCACAGCGGCGACGTGTG 1461

Qy     1441 CACTGCGGCGTCCTTGCCAGTGTTCCAGTCAGTTGATGTGTGGTCAATGATGTGACC    1500
            || |||||||||||||| |||||||||||||||||||||||||| ||||| ||||||
Db     1462 CATTGCGGCGTCCTTGGCCTCCTACCGGAAATGCGCAGTTTGATGTCTGGTCAAACGATGTGACC 1521

Qy     1501 CTGGCCAACCACATGGAGGCAGCAGCCCGGCCTCGGCCTGTGATGGCGGTGCTGGTG    1560
            |||||| ||||||||||||||       |||||||||   |||||||||| ||||
Db     1522 CTGGCTAACCACATGGAGGCCCGGGGGC---GGCCGGCCGCATCCGGGCCAGGCGCGCTACA  1578

Qy     1561 CTGCAGTACCTGAACGCGGGACTACGAGGTGGAGCCAGGCCAGCGGCGCAACGCG       1620
            ||||||||| |||||| |||||| |||||||||||  ||||  |||||| |||||||
Db     1579 CTGCAGTACTTGAACGGGGACTATGAGGTGGAGCGGGTGGAGACGGGTGAACGCAATGCG  1638

Qy     1621 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCGAGAACAACGGAAA 1680
            ||||||||||||||||| |||||||| |||||||| | |||||||  ||| |||||||||||
Db     1639 TACCTCAAGGAGCAGCAGTGCATTGAGACCTTCCTCATACTTGGCGCCGCCAAAAACGGAAA 1698

Qy     1681 GAGGAGAAGGCCATGCTGCGACTCCATGTGGGTGGGTAACGTGCGGTCATCCTGGCG     1740
            |||||||||  |||||||| |||||||  |||||||| ||  |||| ||||| ||||||
Db     1699 GAGGAGAAAGCCATGCTGCCAAGCTTCAGCGGACCTTCAGCGGACACGGGCCTCATGTGGTGGGTGCTGTCTGGCATCCTGCGGCG 1758

Qy     1741 ATGCCCGGCGCTGGGTTCCTGACCCGTGCCTTCTCCCCGGACCAAGGACTCTAAGGACATTCCGC 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1759 ATGCCCGGCGCTGGGTTCCTGACCCGTGCCTTCTCCCCGGACCAAGGACTCTAAGGACATTCCGC 1818
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Qy  1801  CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCCAAGATGCCTGAACCCT  1860
          ||||||||||||||||||||| ||||||||||||||||||  || |||||||||||||
Db  1819  CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCCAAGATGCCTGAACCCT  1878

Qy  1861  GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATGCGCCGAGCCATGATCAGCTG  1920
          ||||||||| |||||||||||||||||||||||||  ||||  |||||||||||||||
Db  1879  GAAGATGAGGTGGATGAGTTCCTGAGCCGTGCCATGCGCCGAGCCATGATCAGCTG  1938

Qy  1921  CGGAAGGACCATGTGCCCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAGAAGAAG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1939  CGGAAGGACCATGTGCCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAGAAGAAG  1998

Qy  1981  TACTCCCGGAAGGTGATCCCCGCTTCGGAGCCTAGTTGCCTGTGTCCCTGTTGGTCTTC  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1999  TACTCCCGGAAGGTGATCCCCGCTTCGGAGCCTAGTTGCCTGTGTCCCTGTTGGTCTTC  2058

Qy  2041  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTTCCACCTGATGCTTCGGGATC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2059  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTTCCACCTGATGCTTCGGGATC  2118

Qy  2101  TATGCCAGCATCTTCCTGCTGCTAATCACGTGCTGATCTGTGTGTACTCCTGT  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2119  TATGCCAGCATCTTCCTGCTGCTAATCACGTGCTGATCTGTGTGTACTCCTGT  2178

Qy  2161  GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCGTCCGCAGCATTGTCCGCTCACGGGCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2179  GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCGTCCGCAGCATTGTCCGCTCACGGGCA  2238

Qy  2221  CATAGCACCGCAGTTGGCATCTTTCCGTGTTGTTACTTCTGCCATTGCCAAC  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2239  CATAGCACCGCAGTTGGCATCTTTCCGTGTTGTTACTTCTGCCATTGCCAAC  2298

Qy  2281  ATGTTCACCTGTAACCACACCCCCATACGGAGAGCTGTGCAGCCGGATGCTGAATTAACA  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2299  ATGTTCACCTGTAACCACACCCCCATACGGAGAGCTGTGCAGCCGGATGCTGAATTAACA  2358

Qy  2341  CCTGCTGACATCACTGCCTGCAGCAGCTCAATTACTCTCTGGGCCCTGGATGCT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2359  CCTGCTGACATCACTGCCTGCAGCAGCTCAATTACTCTCTGGGCCCTGGATGCT  2418

Qy  2401  CCCCTGTGTGAGGGCCACCATGCCCACCTGACGCTTTCCTGAGTACTTCATCGGGAACATG  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2419  CCCCTGTGTGAGGGCCACCATGCCCACCTGACGCTTTCCTGAGTACTTCATCGGGAACATG  2478

Qy  2461  CTGCTGAGTCTTGGCCAGCTGTCTTCCTGCTTCTTGCCACATCAGCAGCATCGGGAAGTTGGCC  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2479  CTGCTGAGTCTTGGCCAGCTGTCTTCCTGCTTCTTGCCACATCAGCAGCATCGGGAAGTTGGCC  2538

Qy  2521  ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTCGGGTCCCCAGCCACC  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2539  ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTCGGGTCCCCAGCCACC  2598

Qy  2581  ATCTTTGACAACTATGACCTACTGCTTGGCGGTCCATGGCTTGGCTTCTTCCAATGAGACC  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2599  ATCTTTGACAACTATGACCTACTGCTTGGCGGTCCATGGCTTGGCTTCTTCCAATGAGACC  2658

Qy  2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGCCCTCAAATATATGACCCCGTGTG  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2659  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGCCCTCAAATATATGACCCCGTGTG  2718

Qy  2701  ATTCTGCTGGTGTTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2719  ATTCTGCTGGTGTTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC  2778

Qy  2761  CGCCTAGACTTCCTCTGGAAACTACAGGCCAACAGGGGAGGGAGGAGGAGGAGCTA  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2779  CGCCTAGACTTCCTCTGGAAACTACAGGCCAACAGGGGAGGGAGGAGGAGGAGCTA  2838

Qy  2821  CAGGCATACAACCGGAGGCTGCTGCATAAACATTCTGCCCAAGGACGTGGCGCCCACTTC  2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2839  CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGCCCACTTC  2898

Qy  2881  CTGGCCCGGAGCGCCGCCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2899  CTGGCCCGGAGCGCCGCCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT  2958

Qy  2941  ATGTTTGCCTCCATTGCCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2959  ATGTTTGCCTCCATTGCCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  3018

Qy  3001  GGTGTGAGTGGCTGCCTGCGGCGTTCTGCTCACCTTGACTGATCATCGCTGACTTTGATGAGATTATCAGC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3019  GGTGTGAGTGGCTGCCTGCGGCGTTCTGCTCACCTTGACTGATCATCGCTGACTTTGATGAGATTATCAGC  3078

Qy  3061  GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3079  GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3138

Qy  3121  TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3139  TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3198

Qy  3181  GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3199  GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3258

Qy  3241  TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTGGCAGGTGTCATCGGGGCTCGG  3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3259  TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTGGCAGGTGTCATCGGGGCTCGG  3318

Qy  3301  AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTTAGTCGTATGGACAGCACG  3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3319  AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTTAGTCGTATGGACAGCACG  3378

Qy  3361  GGGGTCCCCGACGAATCCAGGTGACGACCTGTACCAGGTTCGCCAAGGGC  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3379  GGGGTCCCCGACGAATCCAGGTGACGACCTGTACCAGGTTCGCCAAGGGC  3438

Qy  3421  TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGAGATGACCACCTAC  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3439  TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGAGATGACCACCTAC  3498

Qy  3481  TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3499  TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC  3558

Qy  3541  AAGGTGGGCACT  3552
          ||||||||||||
Db  3559  AAGGTGGGCACT  3570
```

RESULT 8
AAQ42525
ID   AAQ42525 standard; DNA; 4046 BP.
XX
AC   AAQ42525;
XX
DT   25-MAR-2003 (updated)
DT   14-SEP-1993 (first entry)
XX
DE   Cardiac adenylyl cyclase gene.
XX
KW   Regulation; cardiac function; heart; heart failure; ss.
XX
OS   Canis familiaris.
XX
FH   Key   Location/Qualifiers
FT   CDS   131..3627
FT   /*tag= a
XX
PN   EP543137-A1.
XX
PD   26-MAY-1993.
XX
PF   12-OCT-1992; 92EP-0117374.

XX
PR   18-NOV-1991;   91US-0793961.
XX
PA   (AMCY) AMERICAN CYANAMID CO.
XX
PI   Ishikawa Y;
XX
DR   WPI; 1993-168873/21.
DR   P-PSDB; AAR37309.
XX
PT   Purified DNA encoding cardiac adenylyl cyclase - useful to screen
PT   for cpds. which stimulate activity of the cyclase
XX
PS   Claim 1; Fig 2; 34pp; English.
XX
CC   A canine heart cDNA library was constructed in lambda gt10 and was
CC   screened with a 970 bp AatI-HincII fragment from type I adenylyl
CC   cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
CC   cyclase, which has significant homology to other previously known
CC   types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
CC   Positive colonies were subcloned into pUC18 and further subcloned
CC   and sequenced bidirectionally. The 5.4 kb clone was used to
CC   rescreen the library and on overlapping clone contg. the 5' end of
CC   the gene was isolated. Together the two clones cover the complete
CC   canine cardiac adenylyl cyclase gene. The gene is suspected of
CC   being involved in the regulation of cardiac function and it is thought
CC   that decreased activity of adenylyl cyclase in the heart may be a
CC   major factor in the development of heart failure. Thus the adenylyl
CC   cyclase gene is useful to screen cpds. which stimulate the activity
CC   of the cyclase.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match   86.1%;   Score 3057.6;   DB 14;   Length 4046;
Best Local Similarity   91.9%;   Pred. No. 0;
Matches 3264;   Conservative   0;   Mismatches   279;   Indels   9;   Gaps   3;

Qy   1 ATGTCATGGTTAGTTGGCCTTCCTGCTCCTGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   60
          |||||||||| ||||||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db   131 ATGTCGTGGTTTAGTGGGCCTTCCTGCTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT   190

Qy   61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCCACTCGGCGGGCAGGTGGCTTCTCGCACG   120
          |||||||||||||||||||| ||| ||||| |||||||||||||||||||||||||||||||
Db   191 GAACGCAATGGGCAGAAGCGGT---CCACCGCCGGGACTCCGGACCAGTGCTTCTCGCACG   247

Qy   121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCGCACCCAGCCCCACCCCTGCCGGCCCC   180
          ||||||||||||||||||||||||||| |||| || || | ||| |||||| |||||||
Db   248 CCCCGCTATATGAGCTGCCTCCGGGATGCCAGCCCCAGTCCCACCCCCTGCCGGCCTCCC   307

Qy   181 CCTCGGTGCCCCTGGCAGGATGAGCGCCTTCATCCGGACGCCTTCGTTCGAGGGGGCAAGG   240
          |||||||||||||||||||||| ||| |||||||||||| |||| ||| |||||||| ||||
Db   308 CCTCGGTGCCCCCTGGCAGGATGAGCGCCTTCATCCGGACGCCCGGGCAAGGGGCAACG   367

Qy   241 GAGCTGGGGCTGCGGCAGGCCGTCGGGGCCCCTGGGCTTCGAGGATACCGAGGTGACAACGACACGCG   300
          ||||||||||||||||||||| |||||||||||||||||| | || |||||||||| ||||
Db   368 GAGCTGGGGCTGCGGCCGGCGTCGGGGCCCCTGGGCTTCGAGGA---CCATGTCAGCG   424

Qy   301 GGCGGGACCGGCTGAGGTGGCCGCCCCAGACGCGGCGTGCCCAGAGTGGGCGATCCTGCTGGGCGC   360
          ||||||||| |||||||||| |||||| |||| || || ||||||||||| ||||||| ||||||
Db   425 GTTCGGGGCAGCTGAGGTGCCCTGACGTGACCCCGGGAGTGACCCCGGGATCCTGCTGGGCGC   484

Qy   361 CGTCTGGTGCAGGTGTTCCAGTCAAGCAGTTCCGTTCCGAAGCAGTTCCGCTCGGCGAGGCCGTGTAC   420
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db   485 CGTCTGGCCCAGGTGTTCCAGTCAAGCAGTTCCGCTCGGCGAGGCTGAGGCCGTGACT   544

Qy   421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCAGAGCGCTGCTGATGGCGGTGCTGGTG   480
          ||||||||||||| |||||||||||||||||||||| |||||| |||||||| |||||||
Db   545 CAGCGGTACTTCTTTCAGATGAACCAGAGCAGCCAGAGCAGGAGG---GGCCCGGGCCCGCACG   604

Qy   481 CTGCTCACAGCGCGTGCTGCTGGCTTCCACGCGCCACCCGCCCCGCCCTCAGCCTGCCTAT   540
          ||||||||||||||||||||||||| |||||||||||| ||||||||||||||||| |||||
Db   605 CTGCTGACAGCGCGGTGCTGCTAGCCCTTCCATGCTGCGACCTGGCACCTGCCCCCTTCAGCCTGCCTAC   664

Qy   541 GTGGGACTGTTGGCCTGTGCCGCCCGCCCTGTTCGTGTGGGCTCATGTGGTGTGTAACCGG   600
          |||||||||||| |||| ||||||||||||||||||||||| |||||||||||||||||||||||
Db   665 GTGGGCCCTGCTGGCCTGTGCCGCCCACCCCTCTTCGTGCGGCTCATGTGGTGTGTAACCGG   724

Qy   601 CATAGCTTCCGCCAGGAGTCTCGCAGCAGACCCGCAGCCCCTCGGGGCCCTGG   660
          ||||||||||||||||||||||||||| ||||||| ||||||||||||||
Db   725 CACAGCTTTCGCCAGGACTCCATGTCGTCTGGGTGCTGGGGCATCCTTGGCA   784

Qy   661 GCAGTGCAGGTCGGGGCGCTCTCGCAGCAGACCCGCGACCCGCAGCCCCCTCGTGGGGCCCCTGG   720
          ||||||||| || |||||| ||| ||||||||| ||| |||||||||||| |||||||||||||||
Db   785 GCCGTTCAGGTGGGGGTGGGCGGTGCTGGCCAACCCCCCGCAGCCCCCTCGTGGGCCTCTGG   844

Qy   721 TGCCCCTGTGTTCTTTGTCTACATCCGCTACACGCTCTCCCCATCCGCATCCATGCGGGGTGCC   780
          |||| |||||||| ||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Db   845 TGCCCTGTGTGTTTTTGTCTACATCACACGCTCCTACCCATCCTGGCCTGGCAACTAACCGT   904

Qy   781 GTCCTCAGCGGCGGCGCCTGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTTCCTGCTCGCACCAAC   840
          || |||||||||| ||| |||||||||||| ||||||||||||||||||| ||||||| |||||||||||||||
Db   905 GTCTTCAGTGGCTGGCCTGGCCTTTGCATTTGATCTTGATCTTTGATCTTGGCCTGGCAACTCACCGC   964

Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCTGTGTCGTGCCACCAAC   900
          |||| |||||||||| || || |||||| |||| |||||| |||| || || |||||||||||||||
Db   965 GGTGACGCCTTCCTCTGGAAGCAGCTCGGTGCCAACATGCTGCTGTGTTCCTGTGCCACCAAC   1024

Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGAGTGTCTCAGCGCCAGGCCTTTCAGGAG   960
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1025 GTCATTGGCATCTGCACACTACCCCAGCTGAGGTCTCTCAGCGCCAGGCCTTTCAGGAG   1084

Qy   961 ACCCGCGGTTACATCCAGGCCCGGCTTCCACCTGCACGTGCACCTGCCAGCAGCATGAAATCGGCAGGAGGCGG   1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 ACCCGCGGTTACATTCAGGCCCGGCTGCACCTGCACGTGCACCTGCCAGATAGAGAACCGGCAGCAGGAACGG   1144

Qy   1021 CTGCTGCTGTCGGTATTGCCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA   1080
          ||||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   1145 CTGCTGCGTCCGGTGTTGCCCCCAGCATGTTGCCATGGGAGATGAAAGAAGAGATATCAACACA   1204

Qy   1081 AAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC   1140
          ||||||||| |||||||||||||||||||| |||||||||||||||| |||| ||||||||
Db   1205 AAGAAAGAGACATGATGTTCCACAAGATCTACATCCAGAAGACCATGCATGACAATGTCAGCATC   1264

Qy   1141 CTGTTTGCGACAATTGAGGGCTTCACCAGCGTTGCCGGTGCTTCTGCACG   1200
          ||||| |||||||||| |||||||||||||| ||||||||||||||||||||
Db   1265 CTGTTTGCGACAATTGAAGGCTTCACCAGCGTCCGGTGCTTCTGCACG   1324

Qy   1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTGACAAGCTGGCTCGCGGAGAATCACTGC   1260
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1325 GTCATGACCCTGAACGAGCTCTTTGCCCGGTTTGACAAGCTGCTCGCGCGGAAAATCACTGC   1384

Qy   1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGGCCCGG   1320
          ||||||||||||||||| |||||||||||||||||||||||| |||||||||||||||||||
Db   1385 CTGAGGATCAAGATCTTAGGGGACTGTTACTACTGTGTGTCGGGGCTGCCCGAGGGCCCGG   1444

Qy   1321 GCCGACCATGCCCACTCGCTGTGTGGAGATGATGAGGGGTAGACATGATTGAGGGCCATCTCGCTG   1380
          |||||||||||||||| ||||||||||||||||||| | ||||||||||| | ||||||||||||||
Db   1445 GCAGACCATGCCCACTGCCTGTGTGGAGATGATGGGGGTGGACATGATCGAGGGCCATCTCGCTG   1504

Qy   1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGGGCATCCACAGCGGCGCGTG   1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1505 GTGGCGTGAGGTGACAGGTGTGAACGTGAACATGCGGGGCATCCACAGCGGCGGCGTG   1564

Qy   1441 CACTGCGGCGTCCTTGGCTTGCGCGAAATGCAGTTCGATGTGTGGTCCAATGATGTGACC   1500
          ||||||||||||| ||||||||| ||||||||||||||| |||||| |||||||||||||||
Db   1565 CACTGTGGTGTCCTTGGCTTGCGCGGAAATGCAGTTCGACGTGTGGTCCAATGACGTGACT   1624

Qy   1501 CTGGCCAACCAACCACATGGAGGCAGGAGGCCGCTGGCCGCATCCAGAGCTGGCCTGTAC   1560
          ||||||||||||||||| |||||||| ||||| ||||| |||||||||||||||||||||||
Db   1625 CTGGCCAACCAACATGGAGGC---GGCCCGGCCCCGCAATCCAATCCACCCGGCCCACG   1681

Qy   1561 CTGCAGTACCTGAACGGGGACTACGAGGTGGCAAGCGGCCGCTAT   1620
          ||||||||||||||||||||||||||||||||| |||| |||||
Db   1682 CTGCAGTACCTGAACGGGGACTACGAGGTGGCAGCCGGCAACGCG   1741

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Qy  1621 TACCTCAAGGAGCAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCAAACCGAAA 1680
         |||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||
Db  1742 TACCTCAAGGAGCAGCAGCACATCGAGACCTTCCTCATCCTGGGAGCCAGCAAACCGAAA 1801

Qy  1681 GAGGAGAAGGCCATGCTGTGGCCAAGCTGCAGCGGACTCGGCGGACTTCCATGGAAGGCTG 1740
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  1802 GAGGAGAAGGCCATGCTGTGGCCAAGCTGCAGCGGACGCGGCGGACTTCCATGGAAGGCCTG 1861

Qy  1741 ATGCCGCGCTGGGTTCCTGATCGTGCCGTTCTCCCGGACCCAAGGACCCCAAGGCCTTCCGC 1800
         |||| ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db  1862 ATGCCACGCTGGGTGCCCGACCGGCCGCCTTCTCCCGGACCCAAGGACTCCAAGGCTTTCCGC 1921

Qy  1801 CAGATGGGCATTGATGATTCAGCAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1922 CAGATGGGCATTGATGATTCAGCAAGACAACCGGGGTGCCCAAGATGCCCTGAACCCCC 1981

Qy  1861 GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCGCAGCATTGATCAGCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1982 GAGGATGAGGTCGATGAGTTCCTGGGCCGTGCCATCGATGCCGCAGCATCGATCAGCTA 2041

Qy  1921 CGGAAGGACCATGCGGCCCGGTTCTGCGCTTCGGAGCCTAGTTGCCTGTGCCTGTGTCTTC 1980
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  2042 CGGAAGGACCATGCGGCCCGCTTCTGCGCTTCGGAGCCTAGTTGGCTGTGGCTGTGTCTTC 2101

Qy  1981 TACTCCCGGAAGGTGGATCCCCGCTTCATCTGTCATCTTCCCACACTCCACCCTGATGCTTGGGATC 2040
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  2102 TACTCAAGGAAGGTGGACCCCCGCTTCGGAGCCTAGTTGGCTGTGGCTGTGTCTTTGGTCTTC 2161

Qy  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCGATGCTTGGGATC 2100
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  2162 TGCTTCATCTGCTTTATTCAGCTTGTTGCTCTGATCAACCGTGACCGTGCTTGGGATC 2221

Qy  2101 TATGCCAGCATCTTCCTGCTGCTAAGGCCCTGTCGTCCGCGCAGCATGTCTCGGCTCACGGCA 2160
         ||||||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  2222 TACGCAGTATCTTTGCTGTGCTGATCACCGTGACCGTGCCGATCTCGGCCATCGTGTCCGGGCA 2281

Qy  2161 GGTTCTCGTTCCCGTAAGGCCCTGCAGCATCTTCGTCCGCAGCAGTTGTCCGGCTCACGGGCA 2220
         |||||||||||| |||||||||||||||||||||| |||||||||||||||||||||||||||
Db  2282 GGCTTCTCTTCCCCCAAGGGCCCTGCCGACGTCTTTCCCGCAGCATCGTCCGCAGCATCGTGTCCGGGCA 2341

Qy  2221 CATAGCACCGCAGTTGGCATCTTTCGTGCTTGGTTTACTTCTGCCATTGCCAAC 2280
         |||| ||||||||||||||||||  ||||||||| ||||||||||||||||||||
Db  2342 CACAGCACCTGTGTTGGCATTTTTGGCTCTGTCTAGTCGTGTCCATCGCGCCAAC 2401

Qy  2281 ATGTTCACCTGTAAACCACACCACCCCATACGGAGCGTGTCAGCCCGGATGCTGAATTTAACA 2340
         ||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||
Db  2402 ATGTTCACCTGTAAACCACACCACCCCATCCGGACCTGTGCAGCCCGGATGCTGAATGTAACA 2461

Qy  2341 CCTGCTGACATCACTCGCCTGCCAGCTCAATTACTCTCTGGGCCTGATGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2462 CCCGCTGACATCACTCGCCTGCCAGCTCAATTACTCTCTGGGCCTGATGCT 2521

Qy  2401 CCCCTGTGTGAGGGGCACCATGCCCCACTGCCCACCCACTTGCAGCTTCCTCGAGTACTTCATCGGGAACATG 2460
         ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  2522 CCGCTGTGTGAGGGGCACCACCGCCACCCCACTTGCAGCTTCCTCGAGTACTTCGTTGGGGGACATG 2581

Qy  2461 CTGCTGCAGTCTCTTGCCAGCTCGTCCTGCTTCCTGCACACATCGCAGCAGAGTTGGCC 2520
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  2582 CTGCTGCAGTCTCTTGCCAGCTCGTTTCTGCTTCTGCGCACATCGCAGCAGAGTTGGCC 2641

Qy  2521 ATGAATCTTTGTCTTGGGGCTCATCTATTGGTGCTGTTCTGCTTCTGCTGGTCCCCCAGCCACC 2580
         ||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db  2642 ATGAATCTTTGTCTTGGGGCTCATTTATTTGCTGTGTTCTGCTTCTCTGGGCCCCCCAGCACC 2701

Qy  2581 ATCTTTGACAACTATGACCTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2702 ATCTTTGACAACTATGACCTGCTTGGCGTGTCATGGCTTGGCTTCTTCCAATGACACC 2761

Qy  2641 TTTGATGGGCTGGACTGTCGCAGCTGCAGGAGGGGTGGCCCTCAAATATATGACCCCTGTG 2700
         |||||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||
Db  2762 TTTGATGGGCTGGACTGCCAGCTGCACTGACAGTGGCACTGAAATACATGACCCCCGTG 2821

Qy  2701 ATTCTCTGGGTGTTTGCGCTGGCGGCTGTATCTGCATGCTGCAGGTGGAGTCGGCTGCC 2760
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Db  2822 ATTCTGCTGGTGTTTGCCCTGCTGGCCTGTGATCGCGCGCTGATCTGCACGCCCAGGGTTGGAATCAACTGCA 2881

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGCAACAGCAGCAACAGGGGGAAGGAGGATGGAGGAGCTA 2820
         || ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  2882 CGTCTGGACTTCCTCTGGAAACTGGAGCAGCAGGGGGAGATGAGGAGGAGCTC 2941

Qy  2821 CAGGCATACAACCGGAGCGGCTGCTGCATAACATTCTGCCAAGACGTGGCGGGCCCACTTC 2880
         |||||| |||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  2942 CAGGGCCTACAACCGGAGCGGCTGCTGCATAAACATTCTGCGCCTAAGGACGTGGCTGCCCACTTC 3001

Qy  2881 CTGGCCCGGGAGCGCGCCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2940
         |||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  3002 CTGGCCCGGGAGCGCCGCCGAACCATGAGCTCTACTACCAGTCGTGTGAGTGTGTGGCCGTC 3061

Qy  2941 ATGTTTGCCTCCATTGCCAACTTCTGAGTTCTCATGTGGAGCTGGAGGCAAACAATGAG 3000
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  3062 ATGTTTGCCTCCATTGCCAACTTTCTCATGTGGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3121

Qy  3001 GGTGTGAGTGCCTGCGGCTCGCTGCAGCTGCGACTTTGACTTTGATGAGATTATCAGC 3060
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  3122 GGTGTCGAGTGCCTGCGGCGTGCTGCAGCTGCGACTTTGATGAGATCATCAGC 3181

Qy  3061 GAGGAGCGGTTCCGGCAGCTGCACCTTGTTGTAGCAGATTGGTAGCACCTACATGGCTGCC 3120
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  3182 GAGGACGCGGTTCCGGCAGCTGCACCTTGTTGTAGCAGATTCGGTAGCACGTACATGGCTGCG 3241

Qy  3121 TCAGGGCTGAACGCCAGCACCTACGATCAGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
         |||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  3242 TCGGGCTGAACGCCAGCACCTACGATCAGATCAGGCCGCGCCCCCACATCACTGCCCTGCC 3301

Qy  3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3302 GACTATGCCATGCGGCTCATGGGGCTGAACATGGGCCCAGTTGTGGCAGGCGTCATTCAACAAC 3361

Qy  3241 TTCCAGATGAAGATTGGCTGAACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACACACG 3300
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  3362 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTTGTGGCAGGCGTCATTGGGGCGTCGG 3421

Qy  3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  3422 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3481

Qy  3361 GGGGTCCCGACCAATCCAGTTGTACCCAGGATCCAGGTACCGTCCAAGGGC 3420
         |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  3482 GGGGTTCCTGACCAATCCAGTTGTACCCAGGATCCAGGTTCCAGGTTCTGCCAAACGG 3541

Qy  3421 TACCAGCTGGAGTGTCGAGGGTCGTCAAGTGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC 3480
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  3542 TACCAGCTGGAGTGTCGAGGGTGGTCAAGGTGGTCAAGGGTGAAGGGCAAGGGGAGATGACCACCTAC 3601

Qy  3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCACAAATTCAGCTGAAGGGACC 3540
         ||||||||||||| |||||||||| |||||||||||||||||||||||||||||||
Db  3602 TTCCTCAATGGGGGCCCCCCCAGTTAGCAGACGACGACCAGCTACAAGTTCAGCTGTCAGGACC 3661

Qy  3541 AAGGTGGGCACT 3552
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Db  3662 AAGGTGGGCATT 3673
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OS   Mus musculus.
XX
PN   WO200188188-A2.
XX
PD   22-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-JP04192.
XX
PR   18-MAY-2000; 2000JP-0145977.
XX
PA   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI   Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR   WPI; 2002-034733/04.
DR   P-PSDB; ABB57257.
XX
CC   Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT   expression levels of particular genes defined in the specification or
PT   by determining the expression profile of a gene group comprising these
PT   genes -
XX
PS   Claim 2; Page 1771-1780; 2690pp; English.
XX
CC   The present invention describes a method for examining ischemic
CC   conditions, comprising measuring the expression levels of particular
CC   genes (I) in a test sample or determining the expression profile of a
CC   gene group in the sample comprising genes selected from (I). The method
CC   is useful for examining the ischemic condition (e.g. compressive
CC   ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC   expression levels of particular genes (ABI99202 to ABI99912, encoding
CC   the protein sequences in ABB57020 to ABB57374) or by determining the
CC   expression profile of a gene group comprising these genes. The
CC   expression levels or expression profiles produced by these genes are
CC   used as an indicator when screening for ischaemic condition-improving
CC   drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC   represent PCR primers for a mouse ischaemic condition related sequence,
CC   which are used in the exemplification of the present invention.
XX
SQ   Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

Query Match            79.3%;  Score 2816.2;  DB 24;  Length 5841;
Best Local Similarity  87.8%;
Matches  3120;  Conservative    0;  Mismatches  423;  Pred. No. 0;  Indels  10;  Gaps  4;

Qy     1 ATGTCATGGTTTAGTGGCCTTCGTCCTCTGGTCCTAAAGTGATGAACCGAAAACAGCCTGGGGT 60
           ||||||||||||||||||||||| |||||||||||||| |||||||||||||||||||| ||||
Db    96 ATGTCATGGTTTAGTGGCCTTCCTCGGTTCCCAAAGTGGATGAACGGAAAACAGCTTGGGGG 155

Qy    61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGGTTGGCCACTCGGCGGAAGGTTGGCTTCTCGACG 120
           ||| |||||||||||||||           ||||| |||||||||||  |||||||||||||||| |
Db   156 GAAGGCAATGGGCAGAAGCG---CCCACGCCACGCGGAATCGAGCCAGTGGCTTCTCGCGCA 212

Qy   121 CCCCGGCTATATGAGCTCCGGGATGCAGAGCGCACCCAGCCACCCCTGCGGGGCCCC 180
           || ||||| | |||||||  |  ||| || || |||||||||||||| ||| | |||
Db   213 CCTCGCTACACATGAGCTGCCTCAAGAATGCGGAGCCACCCAGCCACCCCTCCTGCAGCTCAC 272

Qy   181 CCTCGGTGCCCCTGCAGGATGACGCCTTCATCCGGAGGGGGCGGCCCAGGCAAGGGCAAG 240
           ||||||||||||||||||||||  ||||| | |||||||||||||  ||| |||||||||
Db   273 ACTTCGGTGCCCCTGCAGGATGATGAAGCCTTAGGAGACGTTCATCAGGAGGGGCGGCAGGGGTGTG 332

Qy   241 GAGCTGGGGCTGCCGGGCCAGTGCCCGGACCCCGGGTCCCGAGGTACCGAGTGACAACGACAGCG 300
           |||||||||||||||||||||||  || |||||||||| ||||| || |||| |||||||||||||
Db   333 GAGCTGGGGCTGCCGGGCCAGTGCCGTCCGGGGTTTGGGGTTTGGGGTAGACATGGGGGGT 392

Qy   301 GGGCGGCCGACGCGCTGGAGGGCTCAGGTGCCCCGCCGTGCCGCCCGGATCCTGCTGCGGC 360
           |||||| || |  | |||  |   ||||| | | |||| ||| ||| ||||||||||||||
Db   393 GGC---ACAGCTTGGTCACCGCGCCACCGGATCATCGCCTGGGGTTTGGGGTTTGGGGTCAACCGATG 449

Qy   361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGCCCAAGCTGGAGCGGCCTGTAC 420
           ||  ||||| || ||||||||||| ||||||||| ||  |||||||||||||||||||
Db   450 CGGCTTGTGTCGCAGTGTTCCAGTCTAAGCAGTTCCGCTCTGGCCAAGCTGGAGCTGGAGCTGTAC 509

Qy   421 CAGCGGTACTTCTTCCAGATGAACCAGAGAGCCTGACGCTGCTGATGGCGGTGCTGGTG 480
           ||||||||||||||||||||||||||||||| |  | |||||| ||||||||||||||||
Db   510 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCAGCTTCACGCTGCTCATGGCGGTGCTGGTG 569

Qy   481 CTGCTCACAGCGGTGCTGCTGGCTTTCCACGCGCCCCTCAGCCTGCCTAT 540
           ||||||| |||||| ||| |||||||||||||| |||||||||||||| ||
Db   570 CTGCTCATGGCGTGTACTGTTGACTTTCCACGCTGCGGCCTCCCAGCCTCAGCCTGCTTAC 629

Qy   541 GTGGCACTGTTGGCTGCCGCGCCCTTGTTCGTGGGCTCATCGTGGTGTTGTAACCGG 600
           ||||| |||  | |||  | || | ||||| |||| ||||||||||| ||||||||| 
Db   630 GTGGCCCTGCTGACCTGTCGCCTCTTGTCCTTTTTGTGGTACTCATGGTGTGTAACCGA 689

Qy   601 CATAGCTTCCGCCAGACTCCATGTGGTGTGAGTTACGTGGTCTCGGGCATCCTGGCG 660
           || ||||||||||||| |||||||||||| || || |||||| | ||||||| |||
Db   690 CACAGCTTCCGCCAGGACTCCATGTGGTGGAGCTATGTGGTCCTGGGCATCCTAGCA 749

Qy   661 GCAGTGCAGGTCGGGGGCGGCCCTCTCGCAGCAGACCCGCGCAGCCCTCCTGCGGGCTCTGG 720
           || ||||| |||||||| | ||||| ||||||| | ||| | |||| | ||||||| |||||
Db   750 GCCGTGCAAGTCGGGGGGGTGCCCTGCGCAGCCAATCCACACAGCCCCTCGGCGGGCCTTTGG 809

Qy   721 TGCCCTGTGTCTTGTCTTGTCTCATCACTCACATACACTACACTTCTTCCCATTCGCAT 780
           ||||| ||| |||||||||||| ||||| | ||| |||||| |||||||||||||  ||
Db   810 TGCCCGTGTTCTTGTCTTGTCTACATCACCTACACTCTTCTTCCCATTCGCATGCATGCGAGCCCGCA 869

Qy   781 GTCCTCAGCGCGCCTGGGCCTTCCCACTTGATCTTGGCCTGCAACTTAACCGT 840
           | |||||||| ||| ||||||| ||| |||||| ||||| ||||| ||||| |
Db   870 GTACTCAGCGGCCTGGGCCTGGCCTGCCCTCTGCTCTGTTTGATTTTGGGCTGGCCTGGCAGCTCAACAGC 929

Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCCTCGCACCAAC 900
           ||| | ||||||||||||||||||||| ||| |||||| |||| ||||| |||||||
Db   930 AGCGACCCCTTCCTTGGAAGCAGCTCGGTGTCTAACGTGGTCTTCCTCTGCACCAAT 989

Qy   901 GTCATTGGCATCTGCACACCACTATCCAGCAGAGGTGTCTCAGCAGCCTTTCAGGAG 960
           |||||||||||| |||| | | || |||||| |||| |||| |||| | ||||||||
Db   990 GCCATCGGTGTCTGCACACTACCCTGCGTGAAGTGTCTCAGCGCCCAAGCTTTCAGGAG 1049

Qy   961 ACCCGGTTACATCCAGGCCGGGTGCGGCGGCGTCCACTGCACATGAGAATCGGCAGGAGCGCG 1020
           |||||||||||||||||| |||| ||| |||| ||||||||||||||||||| ||| ||||||
Db  1050 ACCGAGTTACATCCAGGCCGGCGGCGGCGTCCACTGCACATGAGAACCGTCAGCAGGAACGG 1109

Qy  1021 CTGCTGCTTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
           ||||||| | | |||||||||||||||||||||||||||| |||||||||||||||||||
Db  1110 CTGCTGCTATCGGTGTTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1169

Qy  1081 AAAAAGAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db  1170 AAAAAGAGAGACATGATGTTCCATAAGATTCCATAAGATTCCAGAAGCATGAGATAATGTCAGCATC 1229

Qy  1141 CTGTTTGCAGACATTGAGGGCTTCACCGAGCTCCCAGTGCGCATCCCAGTCGCGGAGAGTG 1200
           ||| ||||||||||||||||||| ||| ||| ||||||| | |||||||| | ||||| ||
Db  1230 CTGTTTGCGGACATTGAGGGCTTCACCAGCCTCCCCAGTGCTCAGCCTGGCCTCGCGGAGAACTG 1289

Qy  1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1260
           ||||||||||| ||||||| || | ||| ||| |||||| |||| | |||||| | |||
Db  1290 GTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGT 1349

Qy  1261 CTGAGGATCAAGAGATCTTGGGGGACTGGTTGTACTACTGGTCAGGGCGGCCGG 1320
           ||||| |||||||| ||||| || || |||||||||||| | ||||| ||||| 
Db  1350 CTGAGGGATCAAGAGATCTTAGGAGACTGTGCTGTACTACTGCGTGTCCAGGGCTGCCGAGGCCCGG 1409

Qy  1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGCGCCAGGAGCTG 1380
           ||| | ||| |||| || | | |||| || ||| ||||||| | ||| |||||
Db  1410 GCAGATCACGCCCACTGCTGTGTGTGGGGTAGACATGGGGGTAGACATGCGCTGCGTTCGCTG 1469

Qy  1381 GTACGTGAGGTGACAGGTTGGAATGTGAACATGCGGCGCGTG 1440
           ||| | || || |||| | || |||||| |||| || ||| |
Db  1470 GTGGCGTGAGGTAACAGGTGAACGTGAACATGCGCATCCACAGCGACGTGTG 1529

Qy  1441 CACTGCGGTCCTTGGCTTGCGGAAATGCCGAGGCCTGTAC 1500
           || || || |||||||||  | ||||||| ||||| ||||
Db  1530 CATTGCGGCGTCCTTGGCTTCCGCCTACGGAAATGCCGAGGCCTGTAC 1589

Qy  1501 CTGGCCAACCACATGGAGGCAGGAGGCCCGGGCTGCGCCATCCAATCACTCGGGCAACA 1560
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Qy   1590 ||||| ||||||||||||| || ||||| | |||||||||||||| |||||||||
Db   CTGGCTAACCACCATGACTGAGGCCGCGGGGGC---GGCCGGCGCATCCACATCCACTCGGCGCTACA 1646

Qy   1561 CTGCAGTACCTGACACGGGACTACGAGGTGAGCCAGGCCGGTGGTGGCGACGCGCAACGCG 1620
Db ||||| ||||||||||||||||| ||||||||||||||||| ||| |||||||||
              CTGCAGTACTTGAACGGGGACTATGAGGTGGAGCCAGGCCGGTGGTGGTGAACGCAATGCG 1706

Qy   1621 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCTGGGCGCCAGCAGACCCAAAACGGAAA 1680
Db |||| |||||||||||||| ||||||| |||||||||||||||||||||| ||||||||||
              TACCTCAAGGAGCAGTCATTGAGACCTTTCCTCATACTTGGCGCCAGCCCCAAAAACGGAAA 1766

Qy   1681 GAGGAGAAGGCCATGTGCCAAGCTGCAGCGGACTCGGCGACTTCCATGGAAGGGCTG 1740
Db |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
              GAGGAGAAAGCCATGTGCCAAGCTTCAGCGGACACGGGCCAAGCGTTCAGCGGACTG 1826

Qy   1741 ATGCCCGCTGGGTTCCTGATCGTGCCTTCCCGGGACCAAGGACCTTCCGC 1800
Db |||| |||||||||||||||||||||||||||| ||||||||||||||||
              ATGCCCGCTGGGTTCCTGACCGGTTGCTGCATAACCATTCTTCCCAAGGAGCTCAAGGCCATTCCGC 1886

Qy   1801 CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCCGGAGATGCCCTGAACCCT 1860
Db |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
              CAGATGGGCATTGATGATTCAGCAAAGACACACCGGGGTGCCCAAGATGCTCTGAACCCT 1946

Qy   1861 GAGGATGAGGTGGATGAGTTCCTGACGCCGTCGCCATCGATGCCGCAGCATTGATCAGCTG 1920
Db | ||||||||||||||| ||||||| ||||||| |||| |||||||||||||||||||
              GAAGATGAGGTGGATGAGTTCCTGACCCGAGCCATCGATGCCGAAGCATCGGGAGATT 2006

Qy   1921 CGGAAGGACATCTTCCTGCGCCGGTTTCGCGTGGATCTTCAGAGAGAGAAG 1980
Db |||||||||||||||||||| |||||||||||| |||||||||||||||||
              CGTAAGGACATCTTCCTGCTCCTGCTCGTCACTGTGATCTTCCAGAGAGAGAAGAAG 2066

Qy   1981 TACTCCCGGAAGGTGATCGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCTGTTGCTTC 2040
Db || ||||||||||||||||||| ||||||| || |||||| ||| ||||| |||| | |
              TATTCACGGAAGTAGATCCTCGCTTCGGAGCCTACGTCGCCTGTGTCCCTGTTTT 2126

Qy   2041 TGCTTCATCTGCTGCATCTTCTCTCAGCTTCATCTTCATCTTCCACACTTCCACCCTGGATC 2100
Db |||||||||||||| | ||||||||||||||||||||| ||||||||||||| |||||||
              TGCTTCATCTGTTTTATCCAGCCTCCTTGTTCCCATACTTCCACCCCTGATACTCGGGATT 2186

Qy   2101 TATGCCAGCATCTTCCTGCGCTAATCACGGTCGTGTGTTACTCCTGT 2160
Db ||||| |||||||||||||||| || |||||||||| |||||||||||
              TATGCCGCTATCTTCCTGTTGGTCACTGTCGTGTGCCGTGTGCTCCTGC 2246

Qy   2161 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCGTGTCCGCTCACGGGGCA 2220
Db ||||||||||| |||||||||||||||||||||||||| ||||||||||
              GGTTCTTTCTTCCCCAAGGCCCTGCTGTCCCCGCAATATTGTCCGCTCACGGGGTG 2306

Qy   2221 CATAGCACCGAGTTGGCATCTTTCGTCTCGTGTTTACTTCTGCCAATTTAACA 2280
Db |||| ||||||||||| ||||| ||||||||| |||||||||||||||||||
              CACAGCACCGCGGTTGGAATCTTCGTGGTTCGTGCGTTCATCCTGCCATCGCCAAC 2366

Qy   2281 ATGTTCACCTGTAACCACACCCCATACGGAGCGTGTGCAGCCCGGATGCTGAATTTAACA 2340
Db ||||| |||||||| ||||||||||| |||||||||||| | ||||||||||||||||
              ATGTTTACCTGTAATCACACACCCCTGCCCGCGGCGGCCAATAAGAACTAAC 2426

Qy   2341 CCTGCTGACATCACTGCCTACTGTTCTCTCGGGCCTGATGCT 2400
Db |||||||||||||||||||||| ||||||||| ||||||||||
              CCAGCCGGATGTCACCGCGCTGCCTCACAACGCTCAATTACTCTCTCTGGGACTGGATGCT 2486

Qy   2401 CCCCTGTGTGAGGGCCCCAGCAGTTAACAGGCCCAGCCAC-AAATTCAGCTGAAGGGAC 2460
Db |||||| | ||||||| |||||||| || |||||||||||||||||||||||| |||||
              CCCCTGTGTGAGGGCCACCATGCCCACCTGCCACCCACCGAGCTTCCGCAAGGGGAACGTG 2546

Qy   2461 CTGCTGAGTCTTCTGGCCAGTCTGTCTTCTGCACATCAGCAGCATGGGGAAGTTGGCC 2520
Db |||||||||| | ||||||||||||||||||||| ||| ||| ||||||||||||||
              CTGCTGAGTCTTCTCTAGCCAGTCTCTGCTCTTTGTGCTGCTGTTTGCTGCTGGGTCGCTGTGGTCTGGGGT 2606

Qy   2521 ATGATCTTTGTCTTGGGGCTCATCTATTTTGGTCTCTGCTTCTGCTGCTGTGCTTCCAGCCACC 2580
Db |||||||||||||||||||||| | ||||||||||||||||||||
              ATGACCTTCATCTTGGGGTTCACCTACTTTGGTCTTTGCTGCTGTGTGCTGGGTCCCGGCCGCC 2666

Qy   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTTCCATGGCTTCGTTCTTCCAATGAGACC 2640
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2667 ATCTTTGACAACTATGATCTACTGCTGTGGCGTTCCATGGCTTCGTTCTTCCCAATGAGACC 2726

Qy   2641 TTTGATGGGCTGGACTGTCCAGCTGCGCTGGAGGAGGGTGCCCTCAAATATATGACCCCGTG 2700
Db ||||||||||||||| ||||||||||| ||||||||||||||||||||||| |||||||||
              TTTGATGGGCTGGACTGCCCAGCTGTGTCCCTGGAAGGGGTTAGCCGCGTCAAATATATGACCCCCACTTC 2786

Qy   2701 ATTCTGCTGGTGTTTGGCGCTGGCGCTGTATCGTGCATGCGATGGGGAGTGGAGTCGACTGCC 2760
Db ||||||||||||||||||||||| |||||||||||||||||| |||||||| ||||||||||
              ATTCTGCTGGTGTTTGCCCTGGCACTGTTATCCTGCATGTGCATGCGGATCTGGAATCGGACTGCC 2846

Qy   2761 CGCCTAGACTTCCTCTGGAAACTACAGGGCAACAGGGAGAAGGAGGAGGAGGAGCTA 2820
Db ||||||||||||| |||||||||| ||| |||| ||||| |||||| |||||||||||
              CGCCTGGACTTCCTGTGGAAGTTACAGGGCAACAGGGAGAAGGAGGAGGAGGAGCTA 2906

Qy   2821 CAGGCATACAACCGAGGCGTGCTGCATCAACATTCTGCCCAAGGACTCCAAGGCCTTCCGC 2880
Db |||||||||||||||||||| |||||| ||||||| ||||||||||||| |||||||||||
              CAGGCATACAACCGGAGGTTGCTGCATAACATTCTTCCCAAGGACTGGCCCCACTTC 2966

Qy   2881 CTGGCCCGGAGCGCCGCCGCCAATGAGCGCGCCGCAATGAGAACTCTACTATCAGTCGGTGCGTGTGGCTGTT 2940
Db |||||||||| ||||||||||||| |||| |||| |||||||||||| |||||||||||||
              CTGGCCCGGAACGCCGCCGCCAATGTGCGCGCTGCAGTTGATGAGGGCAAACAATGAG 3026

Qy   2941 ATGTTTGCCTCCATTGCTCTCTGAGTTCTATGTGAAGCTGGAGCTGGAAGCAAACAATGAG 3000
Db |||||| |||||||||||| |||| ||||||||| ||| |||||||| |||||||||||
              ATGTTTGCCTCCATCGCTGCCAATTTCTCTGAGTTCTCACGTGGGCTCTCAGGAGCTCGAGGCAAACAACGAG 3086

Qy   3001 GGTGTCGAGTGCTCCTGCGGGGTTTCGCCGGTTCTGCTACCTTCGCGCCGTGAGCAGCTGTGCC 3060
Db |||||||||| ||| |||| ||||||||||||||||||||| || |||||||||||||||
              GGCGTGGAGTGCTCCTGCGGGCTCATGAGATCTCTCAACGAGATCATCAGT 3146

Qy   3061 GAGGAGCGGTTCCGGAGCTGAGCAGCGTCGGATCTGCCCGTGTGCTTGGTGGTTGTTGGTCTTC 3120
Db |||||||||| |||||||||| ||||||| |||| |||||| || |||||||||||||||
              GAGGAGGAATTCCGGAGCTGAGCAGTTGGAGAAGAATCAAGACCATCGGTAGCACCATGGCTGCC 3206

Qy   3121 TCAGGGCTGACGCCAGCACCTAGGATCAGGTGGGCGCCGCTCCACATCACTGCCCCTGCT 3180
Db | |||||| |||||| |||||||||||||||||| ||||||||||||||||||||||||
              TCTGGGCTAAATGCCAGCTATGCCATGAGCCATGGCTCGCTCGGGTGTCGTATGGATGACAGCAGG 3266

Qy   3181 GACTACGCCATGCGGCTGCTCCTGTCGCTGTGATCGTGTCGTGTACTCGT 3240
Db |||||||||||||||| |||| ||||||||||||||| |||||||||||
              GACTATGCCATGCGGCTGCTCCTGGTCTGTGTCTGTGCGCCGTGCTCCTGC 3326

Qy   3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGCCAGTGTCATCGGGGCTCGG 3300
Db ||||||||| ||||| ||||||||||||||||||||||||||| ||||||||||||||
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Qy   3301 AAGCCACAGTATGACATCTGGGGAGGAACACAGTGAAATGTCTCTAGTCGTATGGACAGCACG 3360
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              AAGCCACAGTATGACATCTGGGGAAATACCGTGAATGTTTCCAGTCGTATGGACAGCAGCACT 3446

Qy   3361 GGGGTCCCCGACGAATCCAGGTGACCGAGGTTCTCAGGGC 3420
Db |||||||||||||||||||||| |||||| ||||||||||
              GGAGTTCCTGACCGAATACAGGTGACTACCGAGGTTCTAGCGTGCCAAGGGC 3506

Qy   3421 TACCAGCTGGAGTGTGCAGGGGTGTCAAGGTGAAGGGGAGGATGACCACCCTAC 3480
Db ||||||||||||||||| ||||||||| |||||| |||||||||||||||||||
              TACCAGCTGGAGTGTGGCAGGGGGTGTCAAGGTGAAGGGGAGGATGACCACCCTAC 3566

Qy   3481 TTTCCTCAATGGGGCCCCAGCCAC-AAATTCAGCTGAAGGGAC 3539
Db |||||| ||| ||||||||||||||||||||||||| |||||||
              TTTCCTCAACGCGGGGCCCCAGCGAGTTAGCAGAGTCAACCGAAGGAC 3626

Qy   3540 CAAGGTTGGGCACT 3552
Db |||||| |||||||
              CAAGGTTGGGCATT 3639

RESULT 10
AAA53923
ID   AAA53923 standard; cDNA; 4131 BP.
XX
AC   AAA53923;
XX

```
DT   03-JAN-2001 (first entry)
XX
DE   Type VI adenylyl cyclase coding sequence.
XX
KW   Adenylyl cyclase; type I; type II; recombinant; enzyme; cAMP;
KW   cyclic AMP; adenosine monophosphate; screening; stimulation;
KW   inhibition; treatment; cholera; pituitary tumour; heart failure;
KW   ischaemia; endocrine disorder; cell necrosis;
KW   pseudohypoparathyroidism; endocrine deficiency; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             14..3556
FT                   /*tag= a
FT                   /product= Type VI adenylyl cyclase
XX
PN   US6107076-A.
XX
PD   22-AUG-2000.
XX
PF   04-OCT-1996;   96US-0726214.
XX
PR   04-OCT-1995;   95US-0005498.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Gilman AG, Tang W;
XX
DR   WPI; 2000-578539/54.
DR   P-PSDB; AAB02010.
XX
PT   Novel soluble mammalian polypeptide composition comprising adenylyl
PT   cyclase activity for screening stimulators and inhibitors of adenylyl
PT   cyclase, is activated by Gsalpha
XX
PS   Disclosure; Columns 75-78; 73pp; English.
XX
CC   A recombinant Adenylyl cyclase is described which lacks membrane
CC   bound domains. Separation and purification of the recombinant
CC   enzyme is much easier compared with wild type enzymes and the
CC   recombinant enzyme is more stable than the wild type enzyme which
CC   allows easier screening of compounds that stimulate and inhibit
CC   Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises
CC   a chimera of adenylyl cyclase C 1 and C 2 domains linked covalently.
CC   The domains may be linked by a linker peptide. The recombinant
CC   adenylyl cyclase is useful for screening inhibitors and stimulators
CC   of adenylyl cyclase activity. Inhibitors of the enzyme are useful for
CC   treating cholera, pituitary tumors, heart failure, ischaemia,
CC   endocrine disorders and cell necrosis. Stimulators of adenylyl
CC   cyclase are useful for treating pseudohypoparathyroidism and other
CC   endocrine deficiencies.
XX
SQ   Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Query Match        79.1%;   Score 2810.4;   DB 21;   Length 4131;
Best Local Similarity   87.5%;   Pred. No. 0;
Matches 3110;  Conservative   0;   Mismatches  436;   Indels   8;   Gaps   3;
```

```
Qy     1 ATGTCATGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   60
         ||||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||||
Db    56 ATGTCATGTTTAGCGGCCTCCTGGTTCCCAAAGTGGATGAACGGAAAACAGCCTGGGGC  115

Qy    61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTG---CCCACGCGAGCGACCCAGCCCCC  120
         |||| ||||||| |||| |||          |||   |  |  |||  |  || || ||
Db   116 GAACGCAATGGACAGCAAGCG---CCCACGCGCCTGCCTGCTCAAGAATGTGGAGCCCCG  172

Qy   121 CCCGGCTATATGAGCTGCCTCCGGGATGCGAGCGAGAGCCACCCAGCCCCACCCCTGCCCC  180
         |||| | |||| |||||||||| |        ||| ||| |  || ||||  || |||
Db   173 CCCGGCTACATGAGCTGCCTCCTCAAGAATGTGGAGCCCGCCCCACCCCACTCCTGCAGCTCC  232

Qy   181 CCTCGGTGCCCCTGCCAGGATGACGCCTTCATCCGGAGGGCGAGGGGGCAAG  240
         ||||||||||||| ||||||||  |      | ||| |       |||
Db
```

```
Db   233 ACTCCGGTGCCCCTGCCAGGATGAAGCCTTCATCAGGAGGGCTGGCCCCGGAAGGGGTGTG  292
Qy   241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTGGAGGATACCGAGGTGACAACGACAGCG  300
Db   293 GAGCTGGGGCTGCGCGTCAGTGGCCTTGGGCGTTTGATGACACTGAGTG---ACCACACCG  349
Qy   301 GGCGGGACGGCTGAGGTGGCGCCCCACGCGGCTGCCCAGGAGTGGGCGATCCTGCTGGCGC  360
Db   350 ATGGGGACAGCTGAAGTGGCACCCGACACATCGGCTGCCCGGGCGGTCCGTCCTGCTGGCAC  409
Qy   361 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCGCTGTAC  420
Db   410 CGGCTAGCGCAGGTGTTCCAGTGAACCAGTCCCGTCCGCCCAAGCTGGAGCGGTCTGTAC  469
Qy   421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCGCCTCACGCGTGCTGTGGGTGCTGGTG  480
Db   470 CAGCGGGTACTTCTTCCAGATGAACCAGAGCAGCGCCTCACGCTGCTCATGGGCGTGCTTGTG  529
Qy   481 CTGCTCACAGCCGGTGCTGCTGGCTTCCACGCGCACCCGCCCTGCCTCAGCCTGCCTAT  540
Db   530 CTCCTCATGCTGCTACTGTTGACCTTCCACGCGCGCCTGCCCTCAGCCTGCCTTAT  589
Qy   541 GTGGCACTGTTGGCCTGTGCCGCGCCCTGTTCGTGGGGCTCATGGTGGTGTAACCGG  600
Db   590 GTGGCCCTGCTGACCTGTGCCTCCGTCCTTTGTGGTACTCATGTAGTCGTAACCGA  649
Qy   601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAGTTACGTGGTCTCGGGCATCCTGGCG  660
Db   650 CATAGCTTCCGCCAGGACTCCATGTGGGTAGTGAGCTATGTGGTTCTGGGGCATCCTAGCA  709
Qy   661 GCAGTGCAGGTCGGGGGGCCTCTCCAGCAGCAGCAGCAGACCCGCCAGCCCCTCTGG  720
Db   710 GCCGTGCAAGTCGGGGGTGCCCGGGTGCCAGCAGCCTACACCCAGCCAGCGGCCTTTGG  769
Qy   721 TGCCCTGTGTTCTTTGTCTACATCGCTCACTCACACTTCTTCCATTCGTATGCGAGCGGGCC  780
Db   770 TGCCCCGTGTTCTTTGTCTTCGTCTACATCACCTACACACTTCTTCCATTCGTATGCGAGCGGGCC  829
Qy   781 GTCCTCAGCGGCCTGGCCCTCTCAGCATTTGATCTTGGCCTGGCAACTTAACCGT  840
Db   830 GTGCTCAGTGGCCTGGGTCTTTCCACCCCTGCATTTGATTTTGGGCTGGCATCTCAACAAT  889
Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCGGCTGTCTTCCTCGCACCAAC  900
Db   890 GGTGACCCCTTCCTCTTGGAAGCAGCTCGGTGTCTAACGTGGTGTCTCTTCCTGTGCACCAAT  949
Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGAGGTGTCTCAGCGGCCAGGCCTTTCAGGAG  960
Db   950 GCCATCGGTGTCTGCACGCACTACCCGTGAAGTGTCTCAGCGGTCTCAGGCCTTTCAGGAG 1009
Qy   961 ACCCGCGGTTACATCCAGGCCCGGCTGCACCTGACTTGCAGCATGAGAATCGACAGCAGGAACGG 1020
Db  1010 ACCCGTGGTTACATCCAGGCCCGGCTGCACTTGCAGCATGAGAATCGACAGCAGGAACGG 1069
Qy  1021 CTGCTGCTGTGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
Db  1070 CTGCTGCTCGGTGTTGCCCCAGCATGTTGCCATGGAGATGAAATGAAATGAAAGAGGATATCAACACA 1129
Qy  1081 AAAAAAGGAGACATGATGTTCCAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
Db  1130 AAAAAGGAGACATGATGTTCCACAAGATTTACATCCAGAAGCATGACAATGTCAGCATC 1189
Qy  1141 CTGTTTGCAGACATTGAGGGTTCACCAGCTTCACCAGGGCTTGCTTCTCGCACG 1200
Db  1190 CTGTTTGCCGACATTGAGGGTTCACCAGCCTTCACCAGGGCTTGCTTCTCGCACG 1249
Qy  1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1260
Db  1250 GTCATGACCTTGAATGAGCTCTTTGCCCGGTTCGACAAGCTGCTGCGGAGAATCACTGT 1309
Qy  1261 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGGGCTGCCCGAGGGCCCGG 1320
Db  1310 CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGTGTGTCGGGGCTGCGGGGCTGCCCGAGGGCCCGG 1369
```

This page contains a DNA sequence alignment between a query (Qy) and database (Db) sequence, arranged in two columns of paired Qy/Db rows with flanking position numbers.

Left column (positions 1321–2449):

```
Qy  1321  GCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGGCCATCTCGCTG  1380
          |||||||||||| ||||| |||||||||||||||||  ||||||||| |||||||||||||
Db  1370  GCAGACCATGCCCACTCGTGTGGAGATGGGGGTAGACAGTGATCGATCGAGGGCCATCTCGCTG  1429

Qy  1381  GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG  1440
          |||||||||||||||| |||||||||| |||||||| ||||||||||||||||||||||||
Db  1430  GTGCGTGAGGTAACGGGTGTAAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGTA  1489

Qy  1441  CACTGCGGGCGTCCTTGCGTTGCAGTTCGAGTGTGTTCGATGTGTTCCAATGATGTGACC  1500
          |||||||||||||||||| || ||||| |||||||||| |||||||||||||||||||||||
Db  1490  CACTGCGGGCGTCCTTGGTTCGGGGAAATGGCAGTTTGATGTCTGGTCCCAACGATGTGACC  1549

Qy  1501  CTGGCCAACCACCATGAGGCAGGAGGCCGGGCTGGCCGCATCCACATCACTCGGGCAACA  1560
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Db  1550  CTGGCCAACCACCATGAGGCAGGAGGCCGGGGCCGGGCATCCACATCACTCGGGGCCACA  1609

Qy  1561  CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCCGGGCCTGGTGGGCGCGCAACGCG  1620
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1610  CTGCAGTACCTGAACGGGGACTATGAGGTGGAGCCGGGCGCGGTGAGCGCAACGCG  1669

Qy  1621  TACCTCAAGGAGCACAGCACATTGAGACTTCCTCATCCTGGGCGCCAGAAACCGGAAA  1680
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Db  1670  TACCTCAAGGAGCAGTGCATTGAGACCTTCCTCATACTAGGAGCCGCCAGAAACCGGAAA  1729

Qy  1681  GAGGAGAAGGCCATGTGGCCAAGCTGCAGCGGACTCGGCGACCTGCATGGAAGGGCTG  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1730  GAGGAGAAGGCCATGTGGCCAAGCTGGTGGCAGCGGACTCGGCGACCTCCATCGGAAGGACTG  1789

Qy  1741  ATGCCGCCGCTGGGTTCCCGATCGTGCCGCTGTCCCCGGACCTCCGAAGGCCTTCCGC  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1790  ATGCCGCCGCTGGGTTCCCGACCGTGCCTTCTCCCGGACCTCCGAAGGACTCTAAGGCATTCCGA  1849

Qy  1801  CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1850  CAGATGGGCATCGATGACTCTAGCAGAGAAAGGAACCGGGGTCCCCAAGATGCTCTGAACCCT  1909

Qy  1861  GAGGATGAGGTTGGATGAGTTCCTGAGCCGTGCCATCGATGCCGCAGCATTGATCAGCTG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1910  GAGGATGAGGTGGACGAGTTTCTGGGCCGGCCATCGATGCCGAGCATCGACCCAGCTG  1969

Qy  1921  CGGAAGGACCATGTGCGCCGGTTTCTGCGCCACCTTCCAGAGAGAGGATCTTGAGAGAAG  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1970  CGTAAGGACCATGTGCGCCGGTTTCCTGCTCACCTTCACCTTCCAGAGGGGAGGAGAAGAAG  2029

Qy  1981  TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCCTGTTGGTCTTC  2040
          ||||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db  2030  TATTCACGGAAAGTAGACCCTCGTTTCGGAGCCTACGTTGCCCGTGCCCTGTTTTTC  2089

Qy  2041  TGCTTCATCTGCTTCATCCAGCTTCTTCATCTTCCACACTCCACCCTGATGCTTGGGATC  2100
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Db  2090  TGCTTCATCTGCTTCATCCAGCTTCTTCGTCTTCCACACTCCACCCTGATACTCCGGGATT  2149

Qy  2101  TATGCCAGCATCTTCCTGCTGCTAATCACCAGTCGTCGATCTCGTCGTGCTACTCCTGT  2160
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Db  2150  TATGCCGGGGATCTTCCTTTTTTTGCTGCTCACCGTGCTCATCGTGTCGTGCTGCTCCTGT  2209

Qy  2161  GGTTCTCTGTTCCCGGAAGGTGGATCCCCGCTTCGTGTCCGCTCACGGGCA  2220
          |||||||||||||||||||||| | |||||||||||||||||||||||||||
Db  2210  GGGTCTTTTCTTTTTCCCCACGACCCCGTTTCGTGTCCCGCTCACGGGTG  2269

Qy  2221  CATAGCACCGCAGTTGGCATCTTTTCGTCGCTTTGTGTTTTACTTCTGCCATTGCCAAC  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2270  CACAGCACGGCTGTTGGAGTCTTCGTCGTTTGTGTTCATCTCTGCCATTGCCAAC  2329

Qy  2281  ATGTTCACCTGTAACCACACACCCCATACGAGAGCTGTGCAGCCCGGATGCTGAATTTAACA  2340
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Db  2330  ATGTTCACCTGCACACCCCACTACGAGGACCTGTGCGCCCGGATGCTGAACTTAACA  2389

Qy  2341  CCTGCTTGACATCACTGCCTGCCAGCTCAATTACTCTTCCTCGGGCCTGGATGCT  2400
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Db  2390  CCGTCCGATGTGCACCGCGCCTGCCAGCAGTCAATTACTCTTCCTCGGGACTGGAAGCT  2449
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Right column (positions 2401–3538):

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Qy  2401  CCCCTGTGTGAGGGCCACCATGCCCACCTGCCAGCTTCCTGAGTACTTCATCCGGACAACATG  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2450  CCCCTGTGTGAGGGGCCACCGGACCCCACCTGCCAGCTTCCCTGAGTACTTTGTGTCGGGAGTGTG  2509

Qy  2461  CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACTCAGCAGCATCAGCAGCCACC  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2510  CTGCTGAGTCTCTTGGCCAGCTCCGTCTTCCTCCCACATCACCACATCAGCAGCTAGTT  2569

Qy  2521  ATGATCTTTGTCTTGGGGCTCATCATTATTGGTGTGCTCGTGGTCCCCAGCCACC  2580
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Db  2570  ATGACCTTTGTCTTGGGGGTCATCATTTGTGCTTTGTCTGGTCCCCCAGCCACC  2629

Qy  2581  ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGCGTTGGCTTCTTCCAATGAGACC  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2630  ATCTTTGACAACTATGACTATGTCTGCTGCTGGGTAGCCGTTGGCTTCCTCCAATGAGACC  2689

Qy  2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGGTGCCCTCAAATATGACCCCTGTG  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2690  TTCGATGGGCTGGACTGCCCCAGCCGTAGGGAGGGTAGCGCTCAAATACAACACCCCTGTG  2749

Qy  2701  ATTCTGCTGGTGTTGTTGCGCTGGTCGCGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2750  ATTCTCCTCGTGTTCGCCCCTGGCACTGTATCTCATCCTCTCCACTGGGAATCTACCGCC  2809

Qy  2761  CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGAAGAGGAGGATGGAGGAGCTA  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2810  CGCCTCGGACTTCCTCTGTGGAAATGGCAGGCCACAGGGAGGGGGAGAGAGGAGGAGGTG  2869

Qy  2821  CAGGCATACAACCGAGGCGTGCTGCATAAACATTCTGCCCAAGGACGTGGCCGCGCCCACTTC  2880
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Db  2870  CAGGCCTACAACCGGGGCGTGCTGCATAAACATCCTTCCCAAGGACGTGGCTGCCCCCACTTC  2929

Qy  2881  CTGGCCCCGGAGCGGCCGCCAATGATGAACCTCTACTATCAGTCGTGTGAGTGTGGCTGTT  2940
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Db  2930  CTGGGCCCGGAGCGGGCCGCCAACGACCGTGTACTACCAATCCGCAGTGGCTGGCTGGTC  2989

Qy  2941  ATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  3000
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Db  2990  ATGTTTGCCTCCATGCCCAACTTCTCTGAGTTCTATGTGGAACTGGAGGGAACAATGAG  3049

Qy  3001  GGTGTCGAGTGCCTGCGCGCTGCGGGCTTGATGAGATTATCAGC  3060
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Db  3050  GGCGTGGAGTGCCTGCGGCACTGCTCAATGAGATCATCCGGGACTTTGATGAGATCATCAGT  3109

Qy  3061  GAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
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Db  3110  GAGGAGGGTTTCCGGCAGCTGGAGAAGATCAAGAACCATCGGTAGCACTTGGGGGCCGCC  3169

Qy  3121  TCAGGGCTGAACGCCCAGCACCTACGATCAGGTGGGCGCCTCCCACATCACTGCCCTGCT  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3170  TCCGGGCTAAAATGCCAGCACCTATGACACCGCTGAAGTGTTTCCAGCGCCCCTGGCA  3229

Qy  3181  GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3240
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Db  3230  GACTACGCCCATGCGGCTTATGGAGCAAATGAAGCAAATCAACGAACACTCTTTCAACAAC  3289

Qy  3241  TTTCCAGATGAAGAGATTGGCGTGAACATGGGCCCCAGTGCTGTGCATCGGGGCTCGG  3300
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Db  3290  TTTCCAGATGAAGAGATCGGGTTGAACATGGTGCTCGGTTGTGCATTGGGGGCCCCGG  3349

Qy  3301  AAGCCACCAGTATGACATCTGGGGGAACACACAGTCTCTTCAGTCCGTATGGGACAGCACG  3360
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Db  3350  AAGCCACCAGTATGACATCTGGGGGAAACACCGGTGAATGTTTTCCAGCCGTAGCAGCACA  3409

Qy  3361  GGGGTCCCCGACCAATCCAGTGACCGTGACCACCAGGTTCTACCAGGTTCCAAGGGGC  3420
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Db  3410  GGAGTTCCTGACCGGGTGTCGACGGTGGTCAAGGTGACGGCAAGGTCTCTAGCGTCCAAGGGGC  3469

Qy  3421  TACCAGCTGGAGTGTGAGGGTGTCAAGGTGAGGGCCAAGGGGGATGACCACCTAC  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3470  TACCAACTGGAGTGTCGAGGGTGCGTCAAGGTGAGGGGGAAAGGGGAGGGACCACCTAC  3529

Qy  3481  TTCCTCAATGGGGGGCCCCAGCAGTTAACAGGGCCCA--GCCACAAATTCAGCTGAAGGGA  3538
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Db  3530 TTCCTCAATGGGGGCCCCAGCAGTTAGCAGAGCCCACGAGTGGAAATTCAACCAAGGGA 3589
              ||||||||||||||||||||||||||||| ||| ||| |||    |||||| |||||||
Qy  3539 CCAAGGTGGGCACT 3552
              ||||||||||||||
Db  3590 CCAAGGTGGGCACT 3603
```

RESULT 11
AAD08562
ID   AAD08562 standard; cDNA; 1812 BP.
XX
AC   AAD08562;
XX
DT   04-SEP-2001 (first entry)
XX
DE   Human partial cardiac adenylcyclase VI (ACVI) isoform #2 cDNA.
XX
KW   Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW   myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW   adenylylcyclase; adenylate cyclase; cAMP synthetase;
KW   G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW   cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1812
FT   /tag= a
FT   /product= "Human partial cardiac ACVI isoform #2"
FT   /note= "CDS does not include start and stop codon"
FT   /EC_number= "4.6.1.1"
XX
PN   WO20148164-A2.
XX
PD   05-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US35411.
XX
PR   27-DEC-1999; 99US-0472667.
XX
PA   (REGC) UNIV CALIFORNIA.
XX
PI   Hammond HK, Gao M;
XX
DR   WPI; 2001-418260/44.
DR   P-PSDB; AAE04309.
XX
PT   Novel polynucleotide encoding a modified adenylylcyclase polypeptide
PT   useful for enhancing cardiac function in mammalian hearts, and for
PT   treating heart disease, especially congestive heart failure -
PS   Example 5; Page 115-119; 153pp; English.
XX
CC   The present invention relates to methods and compositions for enhancing
CC   cardiac function in mammalian hearts by inserting transgenes encoding
CC   beta-adrenergic signalling proteins (beta-ASP) which increase
CC   beta-adrenergic responsiveness within the myocardium using in vivo
CC   gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC   receptors (beta-AR), adenylylcyclases (also referred as adenylcyclase,
CC   adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC   (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC   in mammalian hearts and for treating heart disease, especially
CC   congestive heart failure. The present cDNA sequence encodes human
CC   partial cardiac adenylcyclase VI (ACVI) isoform which is used for
CC   generating a third beta-ASP transgene, used in the exemplification
CC   of the invention.
XX
SQ   Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;

Query Match   49.6%; Score 1763.4; DB 22; Length 1812;
Best Local Similarity   98.7%; Pred. No. 0;
Matches 1789; Mismatches 0; Conservative 0; Indels 3; Gaps 1;
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Qy  636 TTACGTGGTGCTCGGCATCCTGGCGGCAGTGCAGGTCGGCGGGGCGCTCTCCGCAGAGACCC 695
             ||||||||||||||||||||||||||||||||||||| ||||||| |||| ||||||||||
Db    3 TAACGTGGTGCTCGGCATCCTGGCGGCAGTGCAGGTGCGGCAGTGCGGGGGGCGCTTCGCAGCAGACCC 62

Qy  696 GCGCAGCCCCTGCTGGCGGCCTCTGGTGCCGTGTTCTTTGTCATCGCCTACACGCT 755
             ||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db   63 GCGCAGCCCCTGCTGGCGGCCTCTGGTGCCGTGTTCTTTGTTATACATCGCATACACGCT 122

Qy  756 CCTCCCATCCGATCGGGGCTGGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTT 815
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  123 CCTCCCCATCCGCATGCGGGCTGCCGTCCTCAGCGGGCCTGGGCCTCTCCACCTTGCATTT 182

Qy  816 GATCTTGGCCTGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA 875
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183 GATCTTGGCCTGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA 242

Qy  876 TGTGCTGCTGTTCCTCTGCACCAACGTCATCGGTGGTGCACACACTATCCAGCAGAGGT 935
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  243 TGTGCTGCTGTTCCTCTGCACCAACGTCATCGGTGGTGCACACACTATCCAGCAGAGGT 302

Qy  936 GTCTCAGCGGCCAGGCCTTTCAGGAGACCCGGGTTACATCCAGGCCCGGCTCCACCTGCA 995
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  303 GTCTCAGCGGCCAGGCCTTTCAGGAGACCCGGGTTACATCCAGGCCCGGCTCCACCTGCA 362

Qy  996 GCATGAGAATCGGCAGCAGGAGGCGGCTGCTGCGTGCGTGTCCCAGCACGTTGCCAT 1055
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  363 GCATGAGAATCGGCAGCAGGAGGCGGCTGCTGCGTGCGTATTGCCCCAGCACGTTGCCAT 422

Qy 1056 GGAGATGAAAGAAGACATCAACACAAAAAAGAGAGAACATGATGTTCCACAAGATCTACAT 1115
             |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db  423 GGAGATGAAAGAAGACATCAACACAAAAAAAGAGAAGAAC---ATGTTCCACAAGATCTACAT 479

Qy 1116 ACAGAAGCATGACAAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 1175
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  480 ACAGAAGCATGACAAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 539

Qy 1176 ATCCAGTGCACTGCGCAGGAGCTGGTCATGAGCCCTGAATGAGCTCTTGCCCGGTTTGA 1235
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  540 ATCCAGTGCACTGCGCAGGAGCTGGTCATGAGCCCTGAATGAGCTCTTGCCCGGTTTGA 599

Qy 1236 CAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTG 1295
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 CAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTG 659

Qy 1296 TGTGTCAGGGCTGCCGAGGGCCGGGCCCCGACCATGCCCACCTGTGTGGAGATGGGGGT 1355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 TGTGTCAGGGCTGCCGAGGGCCGGGCCCCGACCATGCCCACCTGTGTGGAGATGGGGGT 719

Qy 1356 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGAATGTGAACATGCG 1415
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  720 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGAATGTGAACATGCG 779

Qy 1416 CGTGGGCATCCACAGCGGCGGCGTGCACTGGCGCGTCCTTGGCGTTGCCGAAATGCAGTT 1475
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  780 CGTGGGCATCCACAGCGGCGGCGTGCACTGGCGCGTCCTTGGCGTTGCCGAAATGCAGTT 839

Qy 1476 CGATGTGTGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGGAGGCCGGGCTG 1535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840 CGATGTGTGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGGAGGCCGGGCTG 899

Qy 1536 CCGATCCACATCACTGCGGCAACACTGCAGTACTGCAGTGGAGGTTGGAGC 1595
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  900 CCGATCCACATCACTGCGGCAACACTGCAGTACTGCAGTGGAGGTTGGAGC 959

Qy 1596 AGGCCGTGTGGGAGCAACGGTACCTCAAGGAGCACATTGAGACTTTCCTCAT 1655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  960 AGGCCGTGTGGGAGCAACGGTACCTCAAGGAGCACATTGAGACTTTCCTCAT 1019

Qy 1656 CCTGGGCGCCAGCAGCCAGAAACGGAAAGAGGAGAGCCATGCTGCCAAGCTGCAGCGGAC 1715
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1020 CCTGGGCGCCAGCAGCCAGAAACGGAAAGAGGAGAGCCATGCTGCCAAGCTGCAGCGGAC 1079
```

```
Qy  1716 TCGGGCCAACTCCATGGAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCG 1775
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1080 TCGGGCCAACTCCATGGAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCG 1139

Qy  1776 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCG 1835
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCG 1199

Qy  1836 GGGCACCCAAGATGCCCTGAGGATGGATGAGTTCCTGAGCCGGTGCCAT 1895
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 GGGCACCCAAGATGCCCTGAGGATGGATGAGTTCCTGAGCCGGTGCCAT 1259

Qy  1896 CGATGCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCCGCGGTTTCTGCTCACCTT 1955
         ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  1260 CGATGCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCCGCGGTTTTTGCTCACCTT 1319

Qy  1956 CCAGAGAGAGGATCTTGAGAAGAAGTACTCCCGGAAGGTGATCCCCGCTTCGGAGCCTA 2015
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1320 CCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGATCCCCGCTTCGGAGCCTA 1379

Qy  2016 CGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCGTGCTTCATCCTCCC 2075
         |||||||||||||||||||||||||||||||||||| |  ||||||||||
Db  1380 CGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCGTGCTTCATCCTCCC 1439

Qy  2076 ACACTCCACCCTGATGCTTGGGATCATGCCAGCATCTTCCTGCTGCTAATCACCGT 2135
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  1440 ACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTAATCACCGT 1499

Qy  2136 GCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTC 2195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1500 GCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTC 1559

Qy  2196 CCGCAGCATTGTCCGCTCACGGGCACATAGCACCGGCAGTTTTTCCGTCCTGCT 2255
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1560 CCGCAGCATTGTCCGCTCACGGGCACATAGCACCGGCAGTTTTTCCGTCCTGCT 1619

Qy  2256 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTG 2315
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1620 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCACCCCCATACGGAGCTG 1679

Qy  2316 TGCAGCCGGATGCTGAATTAACACCTGCTGACATCACTGCCTGCCACCTGCAGCAGCT 2375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1680 TGCAGCCGGATGCTGAATTAACACCTGCTGACATCACTGCCTGCCACCTGCAGCAGCT 1739

Qy  2376 CAATTACTCTCTGGGCCTGGATGCTCCCCGTGTGAGGGGCACCATGCCCACCTGCGACCTT 2435
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1740 CAATTACTCTCTGGGCCTGGATGCTCCCCGTGTGAGGGGCACCATGCCCACCTGCAGCTT 1799

Qy  2436 TCCTGAGTACTTC 2448
         ||||||   |||
Db  1800 TCCTGAGGTGTTC 1812
```

```
RESULT 12
ABS54132
ID   ABS54132 standard; cDNA; 1812 BP.
XX
AC   ABS54132;
XX
DT   20-NOV-2002  (first entry)
XX
DE   Human cDNA encoding partial Adenylylcyclase isoform 6, AC-VI #2.
XX
KW   Human; bs; gene; adenylylcyclase isoform 6; AC-VI; CHF; gene therapy;
KW   beta-adrenergic signalling protein; congestive heart failure; cardiac;
KW   cardiac function; adenovirus vector; transgenic; gene therapy;
KW   beta-adrenergic signalling protein; beta-ASP; heart disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1812
FT                   /*tag= a
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FT                   /EC_number= "4.6.1.1"
FT                   /product= "Partial adenylylcyclase isoform 6"
FT                   /partial
FT                   /note= "No start or stop codon shown"
XX
PN   US200210314 7-A1.
XX
PD   01-AUG-2002.
XX
PF   26-DEC-2000; 2000US-0750240.
XX
PR   27-DEC-1999;    99US-0472667.
XX
PA   (HAMM/)  HAMMOND H K.
PA   (INSE/)  INSEL P A.
PA   (PING/)  PING P.
PA   (POST/)  POST S R.
PA   (GAOM/)  GAO M.
XX
PI   Hammond HK, Insel PA, Ping P, Post SR, Gao M;
XX
DR   WPI; 2002-690626/74.
DR   P-PSDB; ABG32867.
XX
PT   Enhancing cardiac function in a mammal for treating heart disease such
PT   as congestive heart failure, by delivering to the heart of the mammal a
PT   vector comprising a gene encoding a beta-adrenergic signalling protein
PT   .
XX
PS   Claim 75; Page 34-35; 69pp; English.
XX
CC   The invention relates to enhancing cardiac function in a mammal,
CC   involves delivering a vector to the heart of the mammal, where the
CC   vector comprises a gene encoding a beta-adrenergic signalling protein
CC   (beta-ASP) e.g. adenylylcyclase isoform 6 (AC-VI) operably linked to a
CC   promoter. Generating a recombinant replication-defective viral particle
CC   involves introducing first and second plasmids into a replication-
CC   permissive mammalian cell expressing one or more adenovirus genes
CC   conferring replication competence, where the first plasmid comprises a
CC   gene encoding a beta-ASP operably linked to a promoter and further
CC   comprises a replication-defective human adenovirus genome, and the second
CC   plasmid comprises a replication-proficient human adenovirus genome and
CC   further comprises an additional polynucleotide sequence making the second
CC   plasmid too large to be encapsidated in an adenovirus particle, where
CC   rescue recombination takes place between the first plasmid and the second
CC   plasmid to generate a recombinant adenoviral genome comprising the gene
CC   encoding a beta-ASP but lacking one or more adenoviral replication genes,
CC   where the recombinant genome is sufficiently small to be encapsidated in
CC   an adenovirus particle, identifying successful recombinant viral vectors
CC   in cell culture, and propagating a resulting recombinant viral particle
CC   in replication-permissive mammalian cells expressing the missing
CC   adenoviral replication genes to generate a recombinant replication-
CC   defective viral particle. The method is useful for enhancing cardiac
CC   function in a mammal, preferably human and is specifically useful for
CC   treating heart diseases such as congestive heart failure (CHF).
CC   The present sequence is a partial cDNA encoding human Adenylylcyclase
CC   isoform 6, AC-VI, a beta-ASP, used in the method of the invention.
XX
SQ   Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;
```

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Query Match             49.6%;  Score 1763.4;  DB 24;  Length 1812;
Best Local Similarity   98.7%;  Pred. No. 0;
Matches 1789;  Conservative 0;  Mismatches 21;  Indels 3;  Gaps 1;

Qy   636 TTACGTGGTGCTGGGCATCCTGGCGGCGCCTCCGCAGTGCCAGGTCGGGGGCGCGCCGAGACCC 695
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3 TAACGTGGTGCTGGGCATCCTGGCGGCGCCTCCGCAGTGCCAGGTCGGGGGCGCTTCGCAGCAGACCC 62

Qy   696 GCGCAGCCCCCTGCGGGGCCTCTGGTGCCCGTGTTCTTTGTCTACACTCGCCTACACGCT 755
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63 GCGCAGCCCCCTGCGGGGCCTCTGGTGCCCGTGTTCTTTGTCTACACATGCGATACACACGCT 122

Qy   756 CCTCCCCATCCGCATGCGGGGCTGCCGTCCTGCAGGGACGCGGGCCTGGGCCTCTCCACCTTGCATTT 815
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Db 1200 GGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCAT 1259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   123 CCTCCCCATCCGCATGCCGGGCTGCGCCCTGGGCCTCCTCAGCCGGCCTCTCCACCTGCATTT 182

Qy 1896 CGATGCCCGCAGCATTGATCAGTTGCGGAAGGACCACCATGTGCGCCGGCTT 1955
Qy   816 GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA 875
Db 1260 CGATGCCCGCAGCCATTGATCAGTTGCGGAAGGACCACCATGTGCGGCGTTTTGCTCACCTT 1319
Db   183 GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAA 242

Qy 1956 CCAGAGAGAGGATCTTGAGAAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTA 2015
Qy   876 TGTGCTGCTGTTCCTCTGCACCAACGTCATCTGCCATCTGCACACTATCCAGAGAGAGT 935
Db 1320 CCAGAGAGAGGATTTTGAGAAGAGAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTA 1379
Db   243 TGTGCTGCTGTTCCTCTGCACCAACGTCATCTGCCATCTCCACACTATCCAGAGAGAGT 302

Qy 2016 CGTTGCCTGTGCCCGTGTTCTTCTGCTTCATCTGCTTCATCGTCATCTTCCC 2075
Qy   936 GTCTCAGCGCCAGGCCTTTCAGGAGACCCGGCTTACATCCAGGCCCGGCTCCACCTGCA 995
Db 1380 CGTTGCCTGTGCCCGTGTTCTTCTGCTTCATCTGCTTCATCGTCATCTTAATTTTCCC 1439
Db   303 GTCTCAGCGCCAGGCCTTTCAGGAGACCCGGCTTACATCCAGGCCCGGCTCCACCTGCA 362

Qy 2076 ACACTCCACCCTGATGCTTGGGACTATGCCCAGCATCTTCCTGCTGCTAATCACCAGT 2135
Qy   996 GCATGAGAATCGGCAGCAGGCCTGCTGCTGCTGGTATTGCCCCAGCACGTTGCCAT 1055
Db 1440 ACACTTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTAATCACCGT 1499
Db   363 GCATGAGAATCGGCAGCAGGCCTGCTGCTGCTGGTATTGCCCCAGCACGTTGCCAT 422

Qy 2136 GCTGATCTGTGCTGCTACTCCTGTGGTTCTGTCTGTGTCCCTAAGGCCCTGCAAGTCTGTC 2195
Qy 1056 GGAGATGAAAGAAGACATCAACACAAAAAAGAAGACATGATGTTCCAAGATCTACAT 1115
Db 1500 GCTGATCTGTGCTGCTACTCCTGTGGTTCTGTCTGTGTCCCTAAGGCCCTGCAAGTCTGTC 1559
Db   423 GGAGATGAAAGAAGACATCAACACAAAAAAGAAGAC---ATGTTCCAAGATCTACAT 479

Qy 2196 CCGGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT 2255
Qy 1116 ACAGAAGCATGACAATGTCAGCATCCTGTTGCAGACATTGAGGGCTTCACCAGCCTGC 1175
Db 1560 CCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT 1619
Db   480 ACAGAAGCATGACAATGTCAGCATCCTGTTGCAGACATTGAGGGCTTCACCAGCCTGC 539

Qy 2256 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACTGTGACATCACCGAGCTG 2315
Qy 1176 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTGA 1235
Db 1620 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACTGTGACATCACCGAGCTG 1679
Db   540 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTGA 599

Qy 2316 TGCAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCTGCAGCAGCT 2375
Qy 1236 CAAGCTGGCTGCCGGAGAATCACTGCCTGCGGGGATCCTTGTTGTTACTACTG 1295
Db 1680 TGCAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCTGCAGCAGCT 1739
Db   600 CAAGCTGGCTGCCGGAGAATCACTGCCTGCGGGGATCCTTGTTGTTACTACTG 659

Qy 2376 CAATTACTCTCTCGGGCCTGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTT 2435
Qy 1296 TGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCACCATGCCCACCTGCTGTGTGTGTGGGGGT 1355
Db 1740 CAATTACTCTCTCGGGCCTGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTT 1799
Db   660 TGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCACCATGCCCACCTGCTGTGTGTGTGGGGGT 719

Qy 2436 TCCTGAGTACTTC 2448
Qy 1356 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAACATGCG 1415
Db 1800 TCCTGAGGTGTTC 1812
Db   720 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAACATGCG 779

RESULT 13
AAV23246
ID   AAV23246 standard; cDNA; 2127 BP.
XX
AC   AAV23246;
XX
DT   17-JUL-1998 (first entry)
XX
DE   Human adenylylcyclase isoform VI encoding cDNA.
XX
KW   Human; adenylylcyclase VI; AC-VI; beta-adrenergic signalling protein;
KW   transgene; gene therapy; congestive heart failure; cardiac function;
KW   adenovirus; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS
FT   1..2127
FT   /*tag= a
FT   /product= "adenylylcyclase isoform VI"
FT   /transl_except= (pos:229..231,aa:Xaa)
FT   /transl_except= (pos:315..317,aa:Xaa)
FT   /note= "no stop codon given; Xaa = unknown"
FT   misc_difference 315
FT   /*tag= b
FT   /note= "n indicates a gap of about 0.5 kb"
XX
PN   WO9810085-A2.
XX
PD   12-MAR-1998.

Qy 1416 CGTTGGGCATCCACAGCGGCGGCGTGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTT 1475
Qy   780 CGTTGGGCATCCACAGCGGCGGCGTGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTT 839
Qy 1476 CGATGTGTGGTCCAATGATGTGCCCCTGGCCACCACATGGAGGCAGGAGCCGGGGCTGG 1535
Qy   840 CGATGTGTGGTCCAATGATGTGCCCCTGGCCACCACATGGAGGCAGGAGCCGGGGCTGG 899
Qy 1536 CCGGCATCCACATCCACTCGGGCCAACTCGAGTACCTGAACGGGGACTACGGAGGTGGAGCC 1595
Db   900 CCGGCATCCACATCCACTCGGGCCAACTCGAGTACCTGAACGGGGACTACGGAGGTGGAGCC 959
Qy 1596 AGGCCGTGTGGTGGCAAGCGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCAT 1655
Db   960 AGGCCGTGTGGTGGCAAGCGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCAT 1019
Qy 1656 CCTGGGCGTGGTGGCCAGCCAGAAACGCCAGAAACGGAAAGAGGAAGGCCATGCTGCCAAGCTGCAGCCGGAC 1715
Db 1020 CCTGGGCGTGGTGGCCAGCCAGAAACGCCAGAAACGGAAAGAGGAAGGCCATGCTGCCAAGCTGCAGCCGGAC 1079
Qy 1716 TCGGGCCAACTCCATGGAAGGGCTGATGCCGCTGGGGTTCCTGATCGTGCCTTCTCCCG 1775
Db 1080 TCGGGCCAACTCCATGGAAGGGCTGATGCCGATGGGGTTCCTGATCGTGCCTTCTCCCG 1139
Qy 1776 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCG 1835
Db 1140 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCG 1199
Qy 1836 GGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCAT 1895

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XX
PF   05-SEP-1997;   97WO-US15610.
XX
PR   16-JUN-1997;   97US-0048933.
PR   05-SEP-1996;   96US-0708661.
XX
PA   (COLL-) COLLATERAL THERAPEUTICS.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Gao M,  Hammond HK,  Insel PA,  Ping P,  Post SR;
XX
DR   WPI; 1998-193633/17.
DR   P-PSDB; AAW53345.
XX
PT   Vectors containing transgene(s) encoding beta-adrenergic signalling
PT   proteins - useful for gene therapy of congestive heart failure
XX
PS   Claim 60; Fig 12A; 114pp; English.
XX
CC   The present sequence encodes human adenylylcyclase isoform VI (AC-VI)
CC   from the present invention. The present invention describes a
CC   recombinant replication-defective viral particle (I) comprising a gene
CC   encoding a beta-adrenergic signalling protein (beta-ASP) operably
CC   linked to a promoter. Also described are: (1) a recombinant pro-viral
CC   plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
CC   linked to a promoter and further comprising a replication-defective
CC   viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
CC   an isolated polynucleotide comprising a sequence encoding a human
CC   adenylylcyclase isoform VI (AC-VI), or a variant having AC activity;
CC   (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide
CC   sequence which hybridises at high stringency to (3); and (6) a vector
CC   comprising the polynucleotide of (3). (I) can be used to form a
CC   filtered adenovirus particle preparation. (I) is used to enhance
CC   cardiac function in mammals.
XX
SQ   Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

Query Match         49.6%;  Score 1763.4;  DB 19;  Length 2127;
Best Local Similarity   98.7%;  Pred. No. 0;
Matches 1789;   Conservative    0;  Mismatches   21;  Indels   3;  Gaps   1;
```

```
Qy      636 TTACGTGGTGCTGGGCATCCTGGCGCCAGTCGCAGGTCGGGGGCGCTCCGCAGCAGACCC 695
            ||||||| ||| || |||| || |||||||||||||||||||||||||||||||||||||
Db      318 TAACGTGGTGCTGGGCATCCTGGCGCCAGTCGCAGGTCGGGGGCGCTTCGCAGCAGACCC 377

Qy      696 GCGCAGCCCCTCTGCGGGCCTTCGGGGCCCTCTGGTCGCCCGTGTTCTTTGTCTACATCGGCTACACGCT 755
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      378 GCGCAGCCCCTCTGCGGGCCTTCGGGGCCCTCTGGTCGCCCGTGTTCTTTGTCTTTGTATACATCGGCATACACGCT 437

Qy      756 CCTCCCCATCCGCATCGCGGGTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTT 815
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 CCTCCCCATCCGCATCGCGGGTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTT 497

Qy      816 GATCTTGGCCTGGCAACTTAACCGTGGTGATGATGCCTTCCTCGGAAGCAGCTCGGTGCCAA 875
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      498 GATCTTGGCCTGGCAACTTAACCGTGGTGATGATGCCTTCCTCGGAAGCAGCTCGGTGCCAA 557

Qy      876 TGTGCTGCTGTTCCTCTGCACCAACGTCATTGGCATCTGACACACTATCCAGCAGAGGT 935
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      558 TGTGCTGCTGTTCCTCTGCACCAACGTCATTGGCATCTGACACACTATCCAGCAGAGGT 617

Qy      936 GTCTCAGCGCGCCAGGCCTTTCAGGAGACCCGGGCTTACATCCAGGCGCCGGGCTCCACCTGCA 995
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      618 GTCTCAGCGCGCCAGGCCTTTCAGGAGACCCGGGCTTACATCCAGGCGCCGGGCTCCACCTGCA 677

Qy      996 GCATGAGAATCGGCAGCAGGAGAGCGGCTGCTGCTCGGTCGGTATTGCCCAGCACGTTGCCAT 1055
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      678 GCATGAGAATCGGCAGCAGGAGAGCGGCTGCTGCTCGGTATTGCCGGTATTGCCCAGCACGTTGCCAT 737

Qy     1056 GGAGATGAAAGAAGAGACATCAACAAAAAGAAGACATGATGTTCCACAAGATCTACAT 1115
            ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      738 GGAGATGAAAGAAGAGACATCAACAAAAAGAAGAGAC---ATGTTCCCAAGATCTACAT 794
```

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Qy     1116 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 1175
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Db      795 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 854

Qy     1176 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGATGACGTCTTTGCCCGGTTGA 1235
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      855 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGATGACGTCTCTTTGCCCGGTTGA 914

Qy     1236 CAAGCTGGCTGCGGGAGAATCACTCGCTGAGCAAGATCTTGGGGACTGTTACTACTG 1295
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      915 CAAGCTGGCTGCGGGAGAATCACTCGCTGAGCAAGATCTTGGGGACTGTTACTACTG 974

Qy     1296 TGTGTCAGGGCTGCCGGAGGCCCGGACCCGGACCACTGTGTGTGGGAGATGGGGGT 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      975 TGTGTCAGGGCTGCCGGAGGCCCGGACCCGGACCACTGTGTGTGGGAGATGGGGGT 1034

Qy     1356 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATGCG 1415
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1035 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATGCG 1094

Qy     1416 CGTGGGCATCCACAGCGGGCCGTGCACTCGCGGCGTCCTTGGCTTGCGGAAATGGCAGTT 1475
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1095 CGTGGGCATCCACAGCGGGCCGTGCACTCGCGGCGTCCTTGGCTTGCGGAAATGGCAGTT 1154

Qy     1476 CGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGGAGGCGCGGCTGG 1535
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1155 CGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGGAGGCGCGGGCTGG 1214

Qy     1536 CCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGGAGGTGAGCC 1595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1215 CCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGGAGGTGAGCC 1274

Qy     1596 AGGCCGTGGTGGCGGAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTCCTCAT 1655
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1275 AGGCCGTGGTGGCAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCAT 1334

Qy     1656 CCTGGGGCCCAGCAGGAAACCGAAGAAGAGGAGAAGGCCATGCTGGCCAAGCTGCAGCGGAC 1715
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db     1335 CCTGGGGCCCAGCAGGAAACCGAAGAAGAGGAGAAAGGCCATGCTGGCCAAGCTGCAGCGGAC 1394

Qy     1716 TCGGGGCCAACTCCATGGAAGGGCTGAGTGCCGGCTGGGTTCCTGATCGTGCGTTCTCCCG 1775
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1395 TCGGGGCCAACTCCATGGAAGGGCTGAGTGCCGGCTGGGTTCCTGATCGTGCGTTCTCCCG 1454

Qy     1776 GACCAAGGACTTCAAGGCCTTCCGCGAGGCTTCTACATCGGCTACACGGT 1835
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1455 GACCAAGGACTTCAAGGCCTTCCGCGAGGCTTCTACATCGGCTACACGGT 1514

Qy     1836 GGGCACCCAAGATGCCCTGAGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGCCAT 1895
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1515 GGGCACCCAAGATGCCCTGAGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGCCAT 1574

Qy     1896 CGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTCTGCTCACTT 1955
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1575 CGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTGCTCACTT 1634

Qy     1956 CCAGAGAGGATCTTGAGAGAAGAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTA 2015
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1635 CCAGAGAGGATTTTGAGAGAAGAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTA 1694

Qy     2016 CGTTGCCTGTGCCCGTTGGTCTTCTGCTTCATCCGTTCATCTCCC 2075
            |||||||||||||| ||||||||||||||||||||||||||||
Db     1695 CGTTGCCTGTGCCCGTTGGTCTTCTGCTTCATCCGTTCATCTCCC 1754

Qy     2076 ACACTCCACCCTGATGCTTGGGATCTATGCCGACATCTTCCTGCTCGTGCTCATCACCGT 2135
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1755 ACACTCCACCCTGATGTGTTGGGATTTATGCCGACATCTTCCTGCTCGTGCTCATCACCGT 1814

Qy     2136 GCTGATCTGTGTCCGCTCACGGCACATAGACCGAGTTGGCATCTTTTCCGTCCTGCT 2195
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1815 GCTGATCTGTGTCCGCTCACGGCACATAGACCGAGTTGGCATCTTTTCCGTCCTGCT 1874

Qy     2196 CCCGCAGCATTGTCCGCTCACGGCACATAGACCGAGTTGGCATCTTTTCCGTCCTGCT 2255
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CC     isotype of AC5 enables the development of tissue-specific and selective
CC     pharmacological agents for use in treating particular human diseases
CC     associated with hAC5.
XX
SQ     Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;

       Query Match      49.6%;     Score 1761;  DB 20;  Length 4523;
       Best Local Similarity   72.2%;     Pred. No. 0;
       Matches 2385;   Conservative   0;  Mismatches 885;  Indels 33;  Gaps 6;

Qy   214  CGGAGGGGCGGCCCAGGCAAGGCAAGGAGCAGGAGCTGCGGGCAGTGGCCTGGCTTC   273
          ||| ||||| ||||||||||||  |||| ||| ||||||| |||| || |||||||
Db   625  CGGCGGGGCAAGGGGCGGCGGCCGCCGAGCTGGAGCCCGTCGAGGGCGCGGAGCGGAG  684

Qy   274  GAGGATACCGAGTGACAACGACAGCGGGGGACGGCGGGGGACGGGTGGCGCCGACCGGGTG  333
          ||||  |||  | ||||  | ||| | |||||  |||||| |||| || |||| ||||
Db   685  GGGTCCGGGGATGGCGGCAGCTCGGGCTCGGGCTCGGGCTCGGGCTCGGGCGCGGGTG    744

Qy   334  CCCAGGAGTGGGCGGATCCTGCTGCGGCCTGCTTCGTGGCGCGCTCGGTGCAGGTGTTCCAGTCGAAGCAGTTC  393
          |||    ||| |||| || |||| ||||||| || ||| ||| ||| ||| ||||| |||||||
Db   745  C---TGTCCCTGGGCGCCTGCTGCTGGCGTGCTGCAGATATTCCGCTCCAAGAAGTTC  801

Qy   394  CGTTCGGCCAAGCTGGAGCGGCCTGTACCAGCGGTACTTCTTCAGATGAACCAGAGCAGC  453
          |||||| ||||||| |||||||| |||||||||| |||||||||||||| ||||||||||
Db   802  CCGTCGGACAAACTGGAGCCGGCTGTACCAGCGGTACTTCTTCCGCCTGAACCAGAGCAGC  861

Qy   454  CTGACGCTGCTGATGCGGCGTGCTGCTGCGTGCTGCTCCACAGCCGGCTGCTGCTTTCCACGCC  513
          ||| |||||| ||||  |||| |||||||  ||||| || |||| ||||||||| | |||||||
Db   862  CTCACCATGCTCATGGCCGTGCTGGTGCTCGTGTGCTCGTGTGTCATGTTGGCCTTCCACGCG   921

Qy   514  GCACCCGCCGCGCCCTCAGCCTGGCTATGTGGCACTGTTGGCCTGTGCCGTGCCGCCCTGTTC  573
          ||| || || | |||| |||| | ||  |||| || |||| |||| || ||| |||||
Db   922  GCGGCGCCCGCGCCCAGCTGCCTCACCTGGCCGTGCTGGTGCTGGCCGCGCGTCGGGCTGATC   981

Qy   574  GTGGGGCTCATGGTGGTGTAACCGGCATAGCTTCCGCCAGGACTCATGTGGTGGTG  633
          ||| |||| ||||| ||||| ||| ||||||| ||||| |||| ||||||||||
Db   982  CTCATCATGCTGTGCTGTTGCAACCGCGCGCCCTTCCACCAGGACCACATGGGCCTGGCC  1041

Qy   634  AGTTACGTGCTGGCATCCTGGCGGCAGTGCAGGTCGGGGGCGCTCGCAGCAGAC  693
          ||| ||  || || |||| || |||||| || || ||| || || |||| ||
Db   1042 TGCTATGCGGCTCATCGCCGGTGGTGCTGGCCGTCCAGGTGGTGGGGCCTGCTGCCGCAG  1101

Qy   694  CCGCGCAGCCCCTCTGCGGGGCCTCTGCTGTCCTGTGCCCTGTGTCTTGTCTTGTTCTTGTCTGTCACACG  753
          || |||| || || || || || ||| || || |||||| ||||| || |||||||||||
Db   1102 CCACGCAGCCGCCTCTGAGGGCATCTGGACCGTGTTCTCATCTCACCATCCTACACG   1161

Qy   754  CTCCTCCCATCCGCATGGGCGTGCCGTCCTCACGGGGCCTGGGGCCTTCTTCCCACTTTGCAT  813
          |||| || ||| || |||||||  |||| ||| |||  |||| ||| ||| ||||||| ||
Db   1162 CTGCTGCCCGTGCCGCCGCATGCGGCCGCAGTGCTCAGCGGGGTGCTCCTGTCTGCCCCTCCAC   1221

Qy   814  TTGATCTTGGCCAACTTAACCGTGGTGTGATGCCTTCCTGGAAGCAGCTCGGTGCC  873
          |||| || || |||| || ||| ||||| ||| ||| || ||||||||| |||||
Db   1222 CTGGCCATCGCCCTGCGCACCACGCCCAGGACCAGTTCCTGCTGGAAGCAGCTGTCTCC  1281

Qy   874  AATGTCGTCGTGTTCCTCTGCACCAAGTCATTGCACTCGTGGTGTCTGCACTATCCGCAGAG  933
          |||||| ||| || ||| ||||| ||||| || ||||  || ||||| || ||||||||
Db   1282 AATGTTCTCATTTTCTCATTTCCTGCACCATCGTGGGTGTCTGCACCCACTATCCGCTGAG  1341

Qy   934  GTGTCTCAGCGCCAGGCCTTCAGGAGACCCGCGGTTACATCCGGGTCACCCACCTG  993
          ||||| ||||| ||||||  || ||| ||| ||||| |||||||| || |||| ||
Db   1342 GTCTCCCAGAGACAGGCTTTCCAGGAGACCCGAGAGTGCATCCGGCCGCTCCACTCG  1401

Qy   994  CAGCATGAGAATCGCAGCAGGAGGCGGCTGCTGCTCGGTATTGCCCCAGCACGTTGCC  1053
          |||| ||||| |||  |||||| || ||| ||| ||||||| ||||||||| |||||
Db   1402 CAGCGGGAGAACCAGCAGCAGGAACGGGCTCCTGGCTGTGTCCTGTCCCCGTCATGTTGCC  1461

Qy   1054 ATGGAGATGAAAGAAGACATCAACACAAAAAAAGAAGACATGATGTTCCAAGATCTAC  1113
          ||||||||||| |||||||| ||| ||| ||||| ||| ||||| ||||| |||| ||
Db   1462 ATGGAGATGAAAGCAGACATCAACCGCCAAGCAGCAGGAGGATATGATGTTCCATAAGATTTAC  1521

Qy   1114 ATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTG  1173
          || || |||| |||||| || || || |||| || || ||  | |||| |||||||||||
Db   1522 ATCCAGAAACATGCAACGTGAGCATCCTGTTTGCTGACATGCAGGGGCTTCACCAGCCTG  1581
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Db   1875  CCGGAGCATTGTCCGCTCACGGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT  1934
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2256  TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACCACCCCATACGGAGCTG  2315
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1935  TGTGTTTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACCACCCCATACGGAGCTG  1994
Qy   2316  TGCAGCCCGGATGCTGAATTAACACCTGCTGACATCACCTGCCACCTGCAGCAGCT  2375
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1995  TGCAGCCCGGATGCTGAATTAACACCTGCTGACATCACCTGCCACCTGCAGCAGCT  2054
Qy   2376  CAATTACTTCTCTGGCCTTGATGTCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTT  2435
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2055  CAATTACTTCTCTGGCCTTGATGTCCCCTGTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTT  2114
Qy   2436  TCCTGAGTACTTC  2448
                ||||| |||
Db   2115  TCCTGAGGTGTTC  2127
```

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RESULT 14
AAX00462
ID   AAX00462 standard; DNA; 4523 BP.
XX
AC   AAX00462;
XX
DT   25-MAY-1999  (first entry)
XX
DE   Human type V adenylyl cyclase coding sequence.
XX
KW   Type V adenylyl cyclase; human; hAC5; heart disease; brain;
KW   therapy; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9901546-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;  98WO-US13540.
XX
PR   01-JUL-1997;  97US-0886362.
PR   01-JUL-1997;  97US-0070901.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Tomlinson JA;
XX
DR   WPI; 1999-106048/09.
DR   P-PSDB; AAW30600.
XX
PT   Newly isolated and purified human type V adenylyl cyclase (hAC5)
PT   polypeptide - useful for identifying potential therapeutic agents
PT   that modulate hAC5 activity, and for the diagnosis of
PT   hAC5-associated diseases and disorders
XX
PS   Claim 3; Fig 1a-h; 40pp; English.
XX
CC   This sequence encodes the human type V adenylyl cyclase (hAC5) of the
CC   invention. hAC5 has a similar putative structure to other adenylyl
CC   cyclase isoforms but, like type VI, is distinguishable in that it has a
CC   larger N-terminus and a relatively shorter C-terminus as it lacks the
CC   C2b region. The hAC5 polypeptides are useful in assays that screen for
CC   potential therapeutic agents, which modulate hAC5 activity. These
CC   polypeptides are also useful in assays for the diagnosis of diseases and
CC   disorders. Agonists of hAC5 are useful control agents in such assays, and
CC   they may have useful effects in vivo for treating disease. Antibodies
CC   useful in immunoassays for hAC5. (Ant)agonists are particularly useful in
CC   acting as (ant)agonists have diagnostic and therapeutic effects, and are
CC   treating diseases caused by abnormal hAC5 activity (e.g. in the heart and
CC   brain), and in diseases, which are alleviated by modulating hAC5
CC   activity. The oligonucleotides are useful in methods that inhibit or
CC   regulate hAC5 expression in vivo and in vitro. The cloning of the human
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Right column:

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Qy  2242 TTTTCCGTCCTGTTGTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACC 2301
         ||| ||||||||  || || || ||||||||||||||| ||||| |||||  |||||
Db  2656 TTCACCATCACCCTGGTGTTCCTGGCGTTTTGTCAACATGTTCACGTGCAACTCCAGG 2715

Qy  2302 CCCATACGGAGCTGTGCAGCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGC 2361
         |||||  || || || ||| || || |||| ||||| |||||  ||||| ||||||
Db  2716 GACCTGCTGCGGCTGCTGGCACAGGAGCACAACATCAGCGGCAGCCAGGTCAACGCCGT 2775

Qy  2362 CACCTGCAGCAG------CTCAATTACTCTCTGCGGCCTGGATGCTCCCCTGTGTGAGGGC 2415
         |||||||||||      ||  || ||  |||||||||| || |  |||||| ||||||||
Db  2776 CACGTGGCGGAGTCGGCCGTCAACTACAGCCTGGGCGATGAGCAGGGCTTCTGTGTGGCAGC 2835

Qy  2416 ACCATGCCCACCTGCAGCTTCTGCTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGTCTCTTG 2475
         ||  || |||  |||| |||  || || ||||| |||  || ||| ||| || |||||||||||
Db  2836 CCCTGGCCCACCTGCCAACTTCCCCGAGTACTTCACCTTCACCTTACAGCGTGCTGCTCAGCCTCTG 2895

Qy  2476 GCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGCAGAAGTTGGCCATGATCTTTGTCTTG 2535
         ||| || || ||||||||| || ||  |||| ||| || |||| || |||||||  |||||
Db  2896 GCCTGCTTCCGTGTTCCTGCAGATCAGCTGCATCGGCAGCAGGAAGCTGGTGTCATGCTGGCCATC 2955

Qy  2536 GGGCTCATCTATTTGGTGCTCGTTCTGCTGGTCTGCCAACCACCATCTTTGACAACTAT 2595
         ||||||||| ||| || |||| |||||| ||||| |  ||| ||  ||||  |||| |
Db  2956 GAGCTCATCTA---CGTGCTCATGGTCGCACGCCCAGGTGTCACGGCTGTCACGGCTTCTTCGACAACGCC 3012

Qy  2596 GACTTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGAC 2655
         ||| |||||| ||||| | || | ||  ||  ||||||     ||  |||||| ||||
Db  3013 GACTTCTGGTCACCGGCCCACCTACAGCTCTTCA---ACAACGGGACCTCCCAGTGC 3069

Qy  2656 TGTCCAGCTGCGAGGGAGGGGTGCCCTCAAATATAGACCCCTGTGATTCTGCTGGTGTTT 2715
         ||| ||||| |||| ||||||  |||| || |||||||||| |||||||| || |||||
Db  3070 CCTGAGCATGCAACCAAGGTGCATTGAAGGTGGTGACGCGCCCATCATCATCTCAGTCTTT 3129

Qy  2716 GCGCGGCTGCGCTGTATCTGCATGTCGCAGCAGCGGGAGAAGGAGGAGCATCAACCGG 2775
         |||| || |||| || ||||||||| ||||||| || |||||||||||||| || ||
Db  3130 GTGCTGGCCCTGTGTACCTGCACGCCCAGCAGCAGTCCTGTGAGTGTGTGGCGGTCGAGTGTCATGTTCGCGTCCCTCGACTTCCTC 3189

Qy  2776 TGGAAACTACAGGCAACAGGGGAGAGGAGGAGGAGCATACAACCGG 2835
         ||||| |||||| || ||||| ||||||||||||| || |||||
Db  3190 TGGAAACTGCAGCCACCAGCCAACAGGGAAAGAGAGGAGGAGCCTACACACCGG 3249

Qy  2836 AGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCCGCCCACTTCCTGGCCCCGGGGAGCGC 2895
         |||||| |  || ||||||| |||||||| ||||| |||||||||||| || |||| || ||
Db  3250 CGGCTGCTGCACAACATCCTGCCCCAAGGACGTGGCCGCCCACTTCACTGGCGCGACGG 3309

Qy  2896 CGCAATGATGAACTCTACTATCAGTCGTGTGAGTCGGTGGCTGGTGTTGCCTCCATT 2955
         |||||||||| |||||| |||||| |||| |||| ||| || ||||||| ||  |
Db  3310 CGCAATGATGAGCTCTACTATCAGTCCTGTGAGTGTCGTGGGCTCATGTCCGCCTCCATC 3369

Qy  2956 GCCAACTTCTCTGAGTTCTATGTGGAGCTGAGTGCGCCGG 3015
         ||||| || || |||||| | |||||| |||||| |||||
Db  3370 GCCAACTTCTCCGAGTTCTACGTGGAGCTGAGTGTGCCTG 3429

Qy  3016 CGGCTGCTCAACGAGATCATCGCTACTTTGATGAGATTCC 3075
         ||||||| |||| |||||| ||| ||||||| |||| ||
Db  3430 CGGCTACTCAATGAGATCATCGCTGATTTGATGAGATATCAGGCTGGTCCGG 3489

Qy  3076 CAGCTCGAAAAGATCAAGAGACGATTGGTAGCAATGGCCTGCTCAGGGGTCGAACGCC 3135
         |||| || ||||||| || ||||| |||||| | |||||||||||| ||| ||||||
Db  3490 CAGCTGGAGAAGATCAAGACCATCAGGCACACCTCACTGGTGCCTCGGCCTCAACGAC 3549

Qy  3136 AGCACCTACGATCAGGTGGGCGCGCTCCACAATCACTGCCCATGCGCG 3195
         || ||||| || |||||||| | ||| || || |||||| || |||
Db  3550 TCTACCTACGAACATGTGGCAAGACCACCACATCAAGGCACCTGCCATGAAG 3609

Qy  3196 CTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATT 3255
         || || || ||||||| |||| |||||| ||  | || |||||| ||||||||||||
Db  3610 CTGATGACCAGACAGATGAAGTACATCAATGAGCACTCCTTCAACAACTTCCAGATGAAGATC 3669

Qy  3256 GGGCTGAACATGGCCCAGTGCCGCCTCCACACCTGCGGGGTCATCGGGC 3315
         |||||| || ||| ||||||| |||| || || |||| |||| || |
Db  3670 GGGCTCAACATCGGCCCCGTGTGGTGCCGGGTGATAGGGGACACGAAAGCCTTCAGTACGAC 3729
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Left column:

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Qy  1174 GCATCCCAGTGCACTGCGCCAGGAGCTGGTCATGACCCTGAATGAGCTCTTGCCCGGTTT 1233
         |||||||| ||||||||| |||||||||| ||||  ||||| ||||| ||||||| ||||
Db  1582 GCGTCCCAGTGCACTGCACGCGACGAACTGGTCATGACCCTCAACGAGCTCTTCGCCCGCTTT 1641

Qy  1234 GACAAGCTGGCTGCGGAGAATCACTGCCTGGAGATCTTGGGGACTGTTACTAC 1293
         ||||||| |||| | |||| ||||||| |||| ||| |||| || || || ||
Db  1642 GACAAGCTGGCCGCGGAGAATCACTGTTTACGTATTAAGATCCTTGGGAATTGTTATTAC 1701

Qy  1294 TGTGTGTCAGGGCTGCGCGAGGCCCGGAGCCCGACCATGCCCACCTGCTGTGTGGAGATGGGG 1353
         || || || ||  ||||| |||| ||  || || || || |  || |||||||||| |||||
Db  1702 TGCGTTCCGGGGCTGCTGAAGCAAGGGCTGACCACCGCCACTGCCCACTGCTGTGTGTGAGATGGGC 1761

Qy  1354 GTAGACATGATTGAGGCCATCTCGCTGGTACGTGACGTGAGGTGACAGGTGAATGTGAACATG 1413
         |  || ||||| |||| |||| |||| ||||||||| ||||| | |||||||||||||||
Db  1762 ATGGACATGATCGAGGCCATCTCGTTGGTTGGTCCCGGAGTGACAGGGGTGAACGTGAACATG 1821

Qy  1414 CGCGTGGGCATCCACAGCGGCGGCGGCCGCGTGCACTGCGCGGTCCTTGGCTTGCGGAAATGGCAG 1473
         ||||| |||||||||||| ||||| || ||  | ||||| |||| ||  |||| ||  ||||| |||
Db  1822 CGTGTGGGAATTCACAGCGGCGGCGGCAGTACAGCTGCGTGTCCTTTGGTCTCAGGAAGTTGCAG 1881

Qy  1474 TTCGATGTGTGTCCAATGATGTGACCCTGGCCAACCACATCAGAGGCAGGAGCCCGGCT 1533
         ||||| ||||| ||   | ||| || || || |||||| || ||  || ||| ||| |
Db  1882 TTCGACGTCTGTCTAACGATGTCACGCTGCTAGCCAACCAACATGAGAGGCTGCGCGCAAGGCA 1941

Qy  1534 GGCCCGATCCACATCACTCGGGCAACACTCGGTCAGTACCTGAACGGGGACTACGAGGTGGAG 1593
         |||||| ||||||||||||||| |||||||  ||||| ||||| || ||| ||||||||||||
Db  1942 GGACGCTGGTCACCGGCCAACGCTACACTCCACTCACTCGATGTGGGGACTACGAGGTGGAG 2001

Qy  1594 CCAGGCCGTGGTGCGGAGCGCCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTCCCTC 1653
         || |||| || | |||||| ||||| |  |||| ||||||||||| ||  |||||| |||
Db  2002 CCAGGCCGTGTGGGGCAACCGCAACCGCTACCTCAAGGAGCAGCAGTACCAGTCTGAAGACCTTCCTC 2061

Qy  1654 ATCCTGGGCGCCAGCCAGAAACGGAAAGAGGAGAAGGCCATGCCTGAACCTGAGCTGCAGCGG 1713
         |||||||||| || || || || |||| |||||||||  |||| || || ||||| |||||||
Db  2062 ATCCTGCGCTGCACCCCAGGAGCTGGAACGCGGCCAGTCCATGCCTGAGATGATGAACCGC 2121

Qy  1714 ACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCTGGGTTCATCGTGCCTTCTCC 1773
         | || ||| ||| ||| || ||||| ||||| |  | ||  |||| |||| ||||
Db  2122 CAGAGAACCAACTCCATGGGACAACCCCACACTGGGGCTGAGCGAGCGCCCCTTCTAC 2181

Qy  1774 --------CGGACCAAGGACTTCCAAGGCCTTCCGCGCCAGATGGCATTGATGATTCC 1821
                 |||| || || |||| ||| |||| |  ||| ||||| ||||| ||||| |
Db  2182 AACCACCTGGGCGTGGGCAACCACAGTGTCCAAGGAGATGGCGGATGGGCTTTGAACAGCCCC 2241

Qy  1822 AGCAAAGACAACGGGGCACCCGGGCTGCCCCAAGATGCCCTGAACCTGAGGTGGATGAGTTC 1881
         || ||||| ||  |||||||| || || |||||| ||||| ||||||| |||||| || ||
Db  2242 A-------AGGACAACGGGGCGCCCAGGCTGCCCGCAGACTGCCTGAGCTGAGGTGGATGAGTTT 2295

Qy  1882 CTGAGCCGTGCTCCCACCCTGCCACCTCCGATCAGCTGCGGAAGGACCATGTGCGCCGG 1941
         |||| ||||| | || |||| |||| ||||| |||||||| || || || |||||| ||
Db  2296 CTGGGCGCCGTGCTCCCCACTCTGGGGTTCGGTCTCTGCAGCACGTCCTGCTGCTG 2355

Qy  1942 TTTCTGCTTCACCTTCCAGAAGAGAGATCTTGAGGAGAAGTACTCCCGGAAGGTGGATCCC 2001
         ||||| ||| || || || ||||| |||  ||||| || ||||| |||||| |||||||
Db  2356 TTCCTGGACCTTTCAGGGAGGCCTGACTTAGAGAAGAAGTACTCCAAGCAGGTGACGACGAC 2415

Qy  2002 CGCTTCGGAGCCTACGTTGCCCTGCCCTGTGTTCATCCGCTTCATCCAG 2061
         || || |||||||| || || |||||| |  || ||  ||||||||||
Db  2416 CGATTTGGTTGGTGTTGTCTGTGATCTCATCACTCCTGCGTCTTTGTCCAG 2475

Qy  2062 CTTCTCATCTTCCCACACTCCACCCTGTGGGATCTATGCCAGCATCTTCCTGCTG 2121
         ||  ||||| |||| ||| |||| | |  ||  ||| |||| ||| ||||||||
Db  2476 ATCACCATCGTCGCCCCACTCCATATTCCATGTGCTTCACTGTTCTCAGCCTGTTCCCTGTG 2535

Qy  2122 CTGCTAATCACCGTCTGCTGATCCTGTCGTGCTCGTGTCTGTACTACTCCTGGTCGTGTCTAACTGGTCTCGGCATC 2181
         ||||| ||||||||||||||| ||||  |||| ||| | || ||||  ||||||||| |||||| ||||||||||
Db  2536 CTGACCTTGGTGTGGTTGTCTCTGTGATCTACTCACCTCCTGCTAAAGCTCTTCCCCCCA 2595

Qy  2182 CTGCTCAACGTCTGTCGTGTCCCGCCATTGTCGCGGCACATAGACCGCAGTTGGCATC 2241
         |||| || || || |||| |||||| || || |||| |||||||  || || |||||
Db  2596 CTGCAGACCCCTTGGTGGTTCTCCAGGAAGATCGAGAAGATGAATGAACCAGACACCCTGGTTGGGTG 2655
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Db    3730  ATCTGGGGCCAATACCGTGAACGTGCCAGCCGCATGGACAGCACCAGCGGTGTACCCGACCGC  3789
                 |||||||| ||||  ||||  ||||| || |||||||||| || |  ||| ||||||||||||||
Qy    3376  ATCCAGGTGACCACCGGACCTGTACCCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGT  3435
                 |||||||| ||| ||| |||||||||||||||||||||||| ||||||||   |||||||||||
Db    3790  ATCCAGGTCACCACCAGACAGATGCTGGCTGCCAACACGTACCAGCTACCAGCTGGAGTGC  3849
Qy    3436  CGAGGGGTGGTCAAGGTCAAGGGGCAAGGGGAGATGACCGAGATGATGACCTCAATGGGGGC  3495
                 ||||||||||||||||||||||||||| ||| ||||| || ||| || ||||||||||||||
Db    3850  CGGGGCGTGGTCAAGGTCAAGGGGCAAAGGCGAGATGATGACCTACTTCCTCAATGGAGGG  3909
Qy    3496  CCC  3498
                 |||
Db    3910  CCC  3912

RESULT 15
AAQ95540
ID    AAQ95540 standard; DNA; 4356 BP.
XX
AC    AAQ95540;
XX
DT    31-JAN-1996  (first entry)
XX
DE    Cardiac adenylyl cyclase gene.
XX
KW    Cardiac adenylyl cyclase; effector enzyme; ss.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             148..3702
FT                    /*tag= a
XX
PN    TW243453-A.
XX
PD    21-MAR-1995.
XX
PF    02-JUL-1992;  92TW-0105242.
XX
PR    12-JUN-1992;  92US-0899068.
XX
PA    (AMCY ) AMERICAN CYANAMID CO.
XX
DR    WPI; 1995-214006/28.
DR    P-PSDB; AAR78519.
XX
PT    Cardiac adenylyl cyclase and corresp. DNA - having specified
PT    sequences
XX
PS    Claim 1; Fig 2; 45pp; Chinese.
XX
CC    AAQ95540 encodes AAR78519, the novel effector enzyme cardiac adenylyl
CC    cyclase.
XX
SQ    Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;

Query Match     49.3%;  Score 1750.8;  DB 16;  Length 4356;
Best Local Similarity   72.3%;  Pred. No. 0;
Matches  2330;  Conservative  0;  Mismatches  876;  Indels  17;  Gaps  4;

Qy     288  GACAACGACAGCGGCGGGCGGGCGGCTGAGGTGGCGCGCCCGACGCGTGCCCAGGAGTGGGCG  347
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Qy     348  ATCCTGCTGGCGCGGCCCGTCTGGTGCAGGTGTTCCAGTGACGGAAGCAGTTCCGTTCGGCCAAGCT  407
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Db     533  --CCTGCTGCCGCGCGCGCTGCTGCAGATCTTCCGCTTCCAAGAAGTTCCCGTCCGACAAGCT  590
Qy     408  GGAGCGGCCTGTACCAGCGGTACTTCTTCAGATGAACCAGAGCAGCCTGCTGAT  467
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Db     591  GGAGCGGGCTGTACCAGCGGTACTTCTTCCGCTTCTTCCGCCTGAACCAGAGCAGCCTTCACCATGCTCAT  650
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Qy	468 GGCGGTGCTGGTGCTGCTCACAGCCGGTGCTGCTCCACGCCGCGCACCCGCGCCC	527
Db	651 GGCCGTGCTGGTGCTGCTGCTCCTTCACGCGCGGCGGCGGGCGCGGCCGCT	710
Qy	528 TCAGCTGCCTATGTGGCACTGTTGCCTGCCGCCGCCTGTTCGTGGGGCTCATGGT	587
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Db	771 GCTCTGCAACCGGCCGCCCGCCTTCCACCAGGACCACATGGGCCTGGCCTGCTACGCGCTCAT	830
Qy	648 GGGCATCCTGCGCGGCAGTGCAGTTCGGGGGCGCCTCGCAGCAGACCCGCGCAGCCCCTC	707
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Db	891 CGAGGGCATCTGGTGGACCGTGTTCTTCATCTACACCATCTACACCCTGCCCGGTGCG	950
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Qy	828 GCAACTTAACGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTGTT	887
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Qy	1008 GCAGCAGGAGACGGCGGCTTCCCTGCTCGTGTCTGTTGCCCAGCACGTTGCCATGGAGATGAAGA	1067
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Qy	1308 GCCGGAGGGCCGCCCGGCCGACCCACTGCTCGTGTGGAGATGGGGTAGACATGATTGA	1367
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Qy	1428 CAGCGGGCGGCGCGTGCACTCGGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGGTC	1487
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Qy	1548 CACTCGGGCAACACTGCAGTACCTGAACGGGACACCTGAACCGGACCCCAGGCCGTGGTGG	1607

This page contains a nucleotide sequence alignment (Db/Qy query-database pairs) with position numbers. The alignment runs in two columns of interleaved Db (database) and Qy (query) sequence blocks with match bars (|).

Left column position labels (ranges):

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Db	1791	...	1850
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Right column position labels (ranges):

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Search completed: January 7, 2004, 02:08:27
Job time : 934 secs

OM nucleic - nucleic search, using sw model

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Run on: January 6, 2004, 23:23:50 ; Search time 12714 Seconds
(without alignments)
11429.211 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	3545.6	99.8	6463	6	AF250226	AF250226 Homo sapi
4	3484.8	98.1	3549	6	AR174473	AR174473 Sequence
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6	3443.2	96.9	3582	6	AX189768	AX189768 Sequence
7	3220.8	90.7	5877	9	AB007882	AB007882 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 10 from Patent WO0148164.
ACCESSION   AX189766
VERSION   AX189766.1 GI:15143139
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Hammond,H.K. and Gao,M.
TITLE   Gene therapy for congestive heart failure
JOURNAL   Patent: WO 0148164-A 10 05-JUL-2001;

Pred. No. is the number of results predicted by chance to have a

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ORIGIN

Query Match        100.0%;  Score 3552;  DB 6;  Length 3552;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3552;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy 1861 GAGGATGAGGTGGATGAGTTCCTGCCGCCGTGCCATGAATGCCCGCAGCATTGATCAGCTG 1920
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Db 1861 GAGGATGAGGTGGATGAGTTCCTGCCGCCGTGCCATGAATGCCCGCAGCATTGATCAGCTG 1920

Qy 1921 CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGAGATCTTGAGAAGAAG 1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGAGGAATCTTGAGAAGAAG 1980

Qy 1981 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCGTTGGTCTTC 2040
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Db   1981  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  2040
           TACTCCCGGAAGGTGGATCCCCGGCTTCGGAGCCTACGTTGCCTGTGCCCGTTGGTCTTC

Qy   2041  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGATC  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGATC  2100

Qy   2101  TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGTGTACTCCTGT  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGTGTACTCCTGT  2160

Qy   2161  GGTTCTCTGTTCCCTAAGGCCCTGCAAGTCTGTCCCGAGCATTGTCCGCTCACGGGCA  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GGTTCTCTGTTCCCTAAGGCCCTGCAAGTCTGTCCCGAGCATTGTCCGCTCACGGGCA  2220

Qy   2221  CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAAC  2280

Qy   2281  ATGTTCACCTGTAACCACACACCCCATACGGAGTGTGCAGCCCGGATGCTGAATTAACA  2340
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Db   2281  ATGTTCACCTGTAACCACACACCCCATACGGAGTGTGCAGCCCGGATGCTGAATTAACA  2340

Qy   2341  CCTGCTGACATCACTGCCTGCGCAGCAGCTCAATTACTCTCTGGCCTGGATGCT  2400
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Db   2341  CCTGCTGACATCACTGCCTGCGCAGCAGCTCAATTACTCTCTGGCCTGGATGCT  2400

Qy   2401  CCCCTGTGTGAGGGCACCATGCCCACCTGCCACCTGCCACCTCATCGGGAACATG  2460
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Db   2401  CCCCTGTGTGAGGGCACCATGCCCACCTGCCACCTGCCACCTCATCGGGAACATG  2460

Qy   2461  CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
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Db   2461  CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520

Qy   2521  ATGATCTTTGTCTTGGGGCTCATCTATTTGTCTGCTGCTTCTGCTGGGTCCCCAGCCACC  2580
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Db   2521  ATGATCTTTGTCTTGGGGCTCATCTATTTGTCTGCTGCTTCTGCTGGGTCCCCAGCCACC  2580

Qy   2581  ATCTTTGACAACAATGACCTACTGCTTGGCGTCCATGGCTTGCCTTCTTCCAATGAGACC  2640
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Db   2581  ATCTTTGACAACAATGACCTACTGCTTGGCGTCCATGGCTTGCCTTCTTCCAATGAGACC  2640

Qy   2641  TTTGATGGGCTGGACTGTGCCAGCTGCAGGGAGGCGTGGGCCCTCAAAATATATGACCCCTGTG  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TTTGATGGGCTGGACTGTGCCAGCTGCAGGGAGGCGTGGGCCCTCAAAATATATGACCCCTGTG  2700

Qy   2701  ATTCTGCTGGTGTTTGCCTGGGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC  2760
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Db   2701  ATTCTGCTGGTGTTTGCCTGGGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC  2760

Qy   2761  CGCCTAGACTTCCTCTGAAAACTACAGGCAACAGGGAGGAGGAGGATGAGAGGAGCTA  2820
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Db   2761  CGCCTAGACTTCCTCTGAAAACTACAGGCAACAGGGAGGAGGAGGATGAGAGGAGCTA  2820

Qy   2821  CAGGCATACAACCGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGCTGTT  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CAGGCATACAACCGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGCTGTT  2880

Qy   2881  CTGGCCCGGAGCGCCGGAGCGTTCAGTTTAGTGCCTCCTGTCCCTAAACTGGATGAACGGAAAAAC AGCCGCGGGGT  2940
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Db   2881  CTGGCCCGGAGCGCCGGAGCGTTCAGTTTAGTGCCTCCTGTCCCTAAACTGGATGAACGGAAAAAC AGCCGCGGGGT  2940

Qy   2941  ATGTTTGCCTCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCCAAACAATGAG  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  ATGTTTGCCTCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCCAAACAATGAG  3000

Qy   3001  GGTGTCGAGTGCTGCCTGCCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC  3060
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Db   3001  GGTGTCGAGTGCTGCCTGCCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC  3060

Qy   3061  GAGGAGCCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
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Db   3061  GAGGAGCCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120

Qy   3121  TCAGGGCTGAACGCAGCAGCACCTACCAGGTGGCCGCGTCCCCACATCACTCGCTCCGGCT  3180
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Db   3121  TCAGGGCTGAACGCAGCAGCACCTACCAGGTGGCCGCGTCCCCACATCACTCGCTCCGGCT  3180

Qy   3181  GACTACGCCATGCGCGGCTCATGGAGCAGCAGATCAATGAGCACTCCTTCAACAAT  3240
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Db   3181  GACTACGCCATGCGCGGCTCATGGAGCAGCAGATCAATGAGCACTCCTTCAACAAT  3240

Qy   3241  TTCCAGATGAAGAGATTGGGCTGAACATGGGCGTGTGCAGGTGTCATCGGGGTCGG  3300
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Db   3241  TTCCAGATGAAGAGATTGGGCTGAACATGGGCGTGTGCAGGTGTCATCGGGGTCGG  3300

Qy   3301  AAGCCACAGTAGATGACATCTGGGGAACACAGTGATGTCTCTAGTGTCGTATGGACAGCACG  3360
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Db   3301  AAGCCACAGTAGATGACATCTGGGGAACACAGTGATGTCTCTAGTGTCGTATGGACAGCACG  3360

Qy   3361  GGGGTCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC  3420
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Db   3361  GGGGTCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC  3420

Qy   3421  TACCAGCTGGAGTGTCGAGGGTGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC  3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421  TACCAGCTGGAGTGTCGAGGGTGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC  3480

Qy   3481  TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCACAAATTCAGCTGAAGGGACC  3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481  TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCACAAATTCAGCTGAAGGGACC  3540

Qy   3541  AAGGTGGCCACT  3552
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Db   3541  AAGGTGGCCACT  3552
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RESULT 2
AR236745
LOCUS         AR236745                4942 bp    DNA            linear    PAT 20-DEC-2002
DEFINITION    Sequence 1 from patent US 6465237.
ACCESSION     AR236745
VERSION       AR236745.1  GI:27280909
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 4942)
  AUTHORS     Tomlinson,J.E.
  TITLE       Cloning and characterization of a human adenylyl cyclase
  JOURNAL     Patent: US 6465237-A 1 15-OCT-2002;
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match             99.8%;  Score 3545.6;  DB 6;  Length 4942;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 3548;  Conservative  0;  Mismatches  0;  Indels  4;  Gaps  0;

Qy     1  ATGTCATGGTTTAGTGCATGTCTCCTGTCCCTAAACTGCTGGATGAACGGAAAAAC AGCCGCGGGGT  60
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Db   145  ATGTCATGGTTTAGTGCATGTCTCCTGTCCCTAAACTGCTGGATGAACGGAAAAAC AGCCGCGGGGT  204

Qy    61  GAACGCAATGGGCAGAGCGTTCGCGCGCCGTGCGCCGTGCGCCGTGCACTTCGCACG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205  GAACGCAATGGGCAGAGCGTTCGCGCGCCGTGCGCCGTGCGCCGTGCACTTCGCACG  264

Qy   121  CCCGCTATATGAGCTGCCTCCGGGATGAGAGCCACCCAGCCGCGGCCCC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   265  CCCGCTATATGAGCTGCCTCCGGGATGAGAGCCACCCAGCCGCGGCCCC  324

Qy   181  CCTCGGTGGCGCCCCTGGCAGGATGACGCCTTCATCCGGACGATTGGCCAAGGCAAG  240
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Db   325 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGGCGGCCCAGGCAAGGGCAAG 384

Qy   241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATGACCGAGGTGACAACGACAGCG 300
         |||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||||||||
Db   385 GAGCTGGGGCTGCGGGCAGTGGCGCTGGGCTTCGAGGATACCGAGGTGCAACGACAGCG 444

Qy   301 GGCGGGACGGCTGAGGTGGCGCCCAGGAGTGGGCGATCCTGCTGCGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 GGCGGGACGGCTGAGGTGGCGCCCAGGAGTGGGCATCCTGCTGCGC 504

Qy   361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGCCAAGCTGAGCGCGCTGTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCGGCCAAGCTGAGCGCGCTGTAC 564

Qy   421 CAGCGGTACTTCTTCAGATGAAACCAGAGCAGCAGCAGCCTGACGCTGCTGATGGCGTGCTGGTG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 CAGCGGTACTTCTTCCGCAGATGAAACCAGAGCAGCAGCAGCCTGACGCTGCTGATGGCGTGCTGGTG 624

Qy   481 CTGCTCACAGCGGTGCTGGCTTTCCACGCCGCACCCGCCCTCAGCCTGCCTAT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 CTGCTCACAGCGGTGCTGGCTTTCCACGCCGCACCCGCCCTCAGCCTGCCTAT 684

Qy   541 GTGGGACTGTGTTCTTGTCTACATCGCTACACGCTCTCCTCCCCATCGCGGGGCTGCC 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 GTGGGACTGTGTTCTTGTCTACATCGCTACACGCTCTCCTCCCCATCGCGGGGCTGCC 744

Qy   601 CATAGCTTCCGCCCAGGACTCCATGTGGGTGGTGACGTTACGTGGTCGTCGGCATCCTGGGCG 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 CATAGCTTCCGCCCAGGACTCCATGTGGGTGGTGACGTTACGTGGTCGTCGGCATCCTGGGCG 804

Qy   661 GCAGTGCAGGTCGGGGGCGCTTCTCGCAGCAGACCCCGCAGCCCCGGCCTCTGG 720
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Db   805 GCAGTGCAGGTCGGGGGCGCTTCTCGCAGCAGACCCCGCAGCCCCGGCCTCTGG 864

Qy   721 TGCCCTGTGTTCTTTGTCTACATCGCTACACGCTCCTCCCCATCGCGGGCTGCC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865 TGCCCTGTGTTCTTTGTCTACATCGCTACACGCTCCTCCCCATCGCGGGCTGCC 924

Qy   781 GTCCTTCAGCCGGCCTGGGCCTGCTTCTCCACCTTGATCTTGGCCAACTTAACCGT 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 GTCCTTCAGCCGGCCTGGGCCTGCTTCTCCACCTTTGATCTTGGCCAACTTAACCGT 984

Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCGTGCCAATGTCGTTCCTCTGCACCAAC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCGTGCCAATGTCGTTCCTCTGCACCAAC 1044

Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCCAGGCCTTTCAGGAG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCCAGGCCTTTCAGGAG 1104

Qy   961 ACCCGCGGTTACATCCAGGCCGCTCCACCTGGGCCCGGCATGAGAATCGGCAGCAGGAGCGG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105 ACCCGCGGTTACATCCAGGCCGCTCCACCTGGGCCCGGCATGAGAATCGGCAGCAGGAGCGG 1164

Qy  1021 CTGCTGCGTCGTATTGCCCCAGCAGCGTTGCGGTGCAAGTGCTGCGGAGAATCACACA 1080
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Db  1165 CTGCTGCGTCGTCGGTTATTGCCCCAGCAGCGTTGCGGTGCAAGTGCTGCGGAGAATCACACA 1224

Qy  1081 AAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 AAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1284

Qy  1141 CTGTTTGCAGACATTGAGGGCTTCACCAGGCTTCACCAGGCCGCTCCAGTGCGCAGGAGCTG 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285 CTGTTTGCAGACATTGAGGGCTTCACCAGGCTTCACCAGGCCGCTCCAGTGCGCAGGAGCTG 1344

Qy  1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTCGCGGAATCACTGC 1260
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Db  1345 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTCGCGGAATCACTGC 1404

Qy  1261 CTGAGGATCAAGACTGTTGGGGGACTGTTACTGTGTGTCAGGGCTGCGCCCGGAGGCCCCGG 1320
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Db  1405 CTGAGGATCAAGACTGTTGGGGGACTGTTACTGTGTGTCAGGGCTGCGCCCGGAGGCCCCGG 1464


Qy  1321 GCCGACCATGCCCACTGCTGTGTGAGATGGGGTAGACATGATTGAGGCATCTCGCTG 1380
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Qy  1381 GTACGTGAGGTGACAGGTGTGAACATGGCGGTGGCATCCACAGCGGCGGCGGTG 1440
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Qy  1441 CACTGCGCGTCCTTGGCTTGGGAAATGCAGTTCGATGTGGTCAATGATGTGACC 1500
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Qy  1501 CTGGCCAACCACATGAGGAGCAGGAGGCCGGCGCATCCATCACTCGGGCAACA 1560
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Db  1645 CTGGCCCAACCACATGAGGAGCAGGAGGCCGGCGCATCCATCACTCCGGCAACA 1704

Qy  1561 CTGCAGTACCTGAACCGGGACTACGAGGTGGAGCTGGTGGTGCAACGCG 1620
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Db  1705 CTGCAGTACCTGAACCGGGACTACGAGGTGGAGCTGGTGGTGCAACGCG 1764

Qy  1621 TACCTCAAGGAGCAGCACATTGAGACTTCCTCATCCTGGGCGCCAGCGAAACGGAAA 1680
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Db  1825 GAGGAGAGAGGCCATGCTGGCCAAGCTGCAGGGACTCGGCGGCGGACTCGGGCAACTCCATGAAGGGCTG 1884

Qy  1741 ATGCCGCGCTGGGTTCCTGATCGTGCTTCTGCGTCCCCGACCAAGGACTCCAAGGCCTTCCGC 1800
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Qy  1801 CAGATGGCATTGATGATTCAGCAAAGACAACCGGGGCACCGGGCACCCAAGAGTGCCCTGAACCCT 1860
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Db  1945 CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCGGGCACCCAAGAGTGCCCTGAACCCT 2004

Qy  1861 GAGGATGAGGTGGATGAGTTCCTGAGCCGGTGCCATGCGATGCCCAGCATTGATCAGCTG 1920
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Qy  1921 CGGAAGGACCATGTGCCGGTTCTGCTGCTCGGTTCCTGTCCTGCTCACCTTCCAGAGAGGAATCTTGAGAAGAAG 1980
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Db  2065 CGGAAGGACCATGTGCCGGTTCTGCTGCTCGGTTCCTGTCCTGCTCACCTTCCAGAGAGGAATCTTGAGAAGAAG 2124

Qy  1981 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGGAGCTACGTTGCCTGTGCCCGTTGGTCTTC 2040
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Qy  2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATCGTGGGGATC 2100
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Db  2185 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATGCCTGGGGATC 2244

Qy  2101 TATGCCAGCATCTTCCTGCTGCTCCAGCACGTTGCCCATCACCGTGCTCGTGTACTCCTGT 2160
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Qy  2161 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCTCAATTGTCCGCTCACGGGCA 2220
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Qy  2221 CATAGACCGCAGTTGGCATCTTTCCGTGTTTACTTCTGCCAAC 2280
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Qy  2341 CCTGCTGACATCACTGCCTGCACCTGACAGCTCAATTACTCTCTGGGGATGCT 2400
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Db        3625 TTCCTCAATGGGCGGCCACT 3684
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RESULT 3
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DEFINITION  Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
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VERSION     AF250226.1  GI:9049782
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6463)
  AUTHORS   Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D.,
            Sarasin,A. and Suarez,H.G.
  TITLE     Cloning and expression of human adenylyl cyclase type VI in normal
            thyroid tissues
  JOURNAL   Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
   MEDLINE   20435313
    PUBMED   10978539
REFERENCE   2  (bases 1 to 6463)
  AUTHORS   Wicker,R., Gascon Catalan,A., Cailleux,A.-F., Starenki,D.,
            Stengel,D., Sarasin,A. and Suarez,H.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
            genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
            CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
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Sequence alignment (Qy = query, Db = database):

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Qy  3121 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACACTGCCCTGGCT 3180
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Qy  3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
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Qy  3421 TACCAGCTGGAGTGTCGAGGGGTCGTCAAGGTGGTCAAGGTGGGAGATGACCACCTAC 3480
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Query Match            99.8%;  Score 3545.6;  DB 9;  Length 6463;
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Qy    121  CCCCGCTATATGAGCTGCCCTGGACGATGACAGCTTCATCCCAGCCCCACCCCTGCGGGCCCC   180
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Qy    181  CCTCGGTGCCCCTGGACGATGGCAGTGACAGTTCCAGTGCGGCTTCGTGCCCAGGGCAAG   240
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Db    875  CCTCGGTGCCCCTGGACGATGGCAGTGACAGTTCCAGTGCGGCTTCGTGCCCAGGGCAAG   934

Qy    241  GAGCTCGGGGCTGCGGGACGGCTGAGTGCGCGCCCACGCGGTGCCCAGCGTCGTGGCGC   300
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Qy    301  GGCGGGACGGCTGAGGTGCGCCCCGACGCGTGCCCAGGAGTGGGCGATCCGTCGTGGCGC   360
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Qy    361  CGTCTGGTGCAGGTGTTCCAGTCGGAAGCAGTTCGGTTCGGCCAAGCTGGAGCGCCTGTAC   420
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Qy    481  CTGCTCACAGCGGTGCTGCTTTCCACGCCGACCCGCACCCGCCCTCAGCCTGCCTAT     540
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Qy    541  GTGGCACTGTTGGCCTGTGCGCGCCGCGCTGTCGTGGGGCTCATGGGCGTCGTGTAACCGG   600
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Db   1235  GTGGCACTGTTGGCCTGTGCGCGCCGCGCTGTCGTGGGGCTCATGGGCGTCGTGTAACCGG  1294

Qy    601  CATAGCTTCCGCCAGGACTCCATGTGGTTACGTGGTGCTGGGGCATCCTGGGCG        660
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Qy    661  GCAGTGCAGGTCGGGGGCGCTTCTCGCAGCAGACCCGCGCAGCCCGCCCTCTCGG       720
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Db   1355  GCAGTGCAGGTCGGGGGCGCTTCTCGCAGCAGACCCGCGCAGCCCGCCCTCTCTG       1414

Qy    721  TGCCCTGTGTCTTTTGTCTACATCGCTACACGCTCTCCCCCATCGCGCATGCGGGGCTGCC   780
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Qy    781  GTCCTCAGCGGCCTGGGCCTTCTCCACTTGGCATTTGATCTTGGCCTGGCAACTTAACCGT   840
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Qy    841  GGTGACCATGTCGCCGTTCGGTGCCAATGTGCTGCTGTTCCTGCACCAAC           900
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Qy    901  GTCATTGGCATCGCACACTACATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG    960
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Db   1595  GTCATTGGCATCGCACACTACATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG   1654

Qy    961  ACCCGGGGTTACATCCAGGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG  1020


Db   1655  ACCCGGGGTTACATCCAGGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG  1714
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Qy   1021  CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCCATGCAGCGTTGCCATGGAGATGAAAGA  1080
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Db   1715  CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCCATGCAGCGTTGCCATGGAGATGAAAGA  1774

Qy   1081  AAAAAGAAGAAACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC  1140
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Db   1775  AAAAAGAAGAAACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC  1834

Qy   1141  CTGTTTTGCAGACATTGAGGGCTTCACCAGGCTTCACCAGCTTGCACTCGCCGAGGACTG  1200
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Db   1835  CTGTTTTGCAGACATTGAGGGCTCTTTGCCGGCTTCACCAGCTTGCACTCGCCGAGGACTG  1894

Qy   1201  GTCATGACCCTGAATGAGCTTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC  1260
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Db   1895  GTCATGACCCTGAATGAGCTTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC  1954

Qy   1261  CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGGCTGCCGAGGGCCCGG  1320
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Db   1955  CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGGCTGCCGAGGGCCCGG  2014

Qy   1321  GCCGACCATGCCCACTGCCTGCTTCGGGCTTGGAGGATACCGAGGTGACAACGACAGCG   1380
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Qy   1381  GTACGTGAGGTGACAGGTGTGAACATGCGGTGGCATCGGCGGGCGGTG           1440
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Db   2075  GTACGTGAGGTGACAGGTGTGAACATGCGGTGGCATCGGCGGGCGGTG          2134

Qy   1441  CACTGCGGGCGTCCTTGGCTTCGATGGTGTTCGATGTGTGGTCAATGATGTGACC        1500
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Db   2135  CACTGCGGGCGTCCTTGGCTTCGATGGTGTTCGATGTGTGGTCAATGATGTGACC       2194

Qy   1501  CTGGCCAACCACATGAGGAGGAGGAGCCGGGCTCGGGGACTCGGCGACTCCATGAAGGGCTG  1560
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Db   2195  CTGGCCAACCACATGAGGAGGAGGAGCCGGGCTCGGGGACTCGGCGACTCCATGAAGGGCTG  2254

Qy   1561  CTGCAGTACCTGAAACGGGGACTACGAGGTGAGCGTGGCGAGCGCAACGCG          1620
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Qy   1621  TACCTCAAGGAGCAGCACATTGAGACTTCCTCATCCTGGCGCCAGCCAGAAACGGAAA   1680
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Db   2315  TACCTCAAGGAGCAGCACATTGAGACTTCCTCATCCTGGCGCCAGCCAGAAACGGAAA  2374

Qy   1681  GAGGAGAAGGCCATGTGGCCAAGCTGCAGCGGACTCGGGGACTCCATGGAAGGGCTG    1740
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Qy   1741  ATGCCGCGCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTTCCAAGGCCTTCCGC  1800
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Qy   1861  GAGGATGAGGTGGATGAGTTCCTGCAGCCTGGCAACTTAACGTGATCAGCTG        1920
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Qy   1921  CGGAAGGACCATGTGCGCCGGTTCTGCTCACCTTCGAGAGGATCTTGAGAAGAAG    1980
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Qy   1981  TACTCCCGGAAGTGGATCGCCCGCTTCGGAGCCTACGTTGCCCGTGCCCTGTTGGTCTTC  2040
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Qy   2041  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCGATGCGTTGGGATC       2100
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Qy  3241 TTCCAGATGAAGATTGGGCTGAACATGGGCGTCGCTGTCGGAGGGTCATCGGGCTCGG     3300
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Db  4115 TACCAGCTGAGTGTGCAGGGGTGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC   4174

Qy  3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540
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RESULT 4
AR174473

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DEFINITION  Sequence 5 from patent US 6306830.
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VERSION     AR174473.1  GI:17914793
KEYWORDS    .
SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 3549)
  AUTHORS   Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.
  TITLE     Gene therapy for congestive heart failure
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BASE COUNT      699 a    1025 c    1061 g     764 t
ORIGIN

Query Match        98.1%;  Score 3484.8;  DB 6;  Length 3549;
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Matches 3517;  Conservative 0;  Mismatches 32;  Indels 3;  Gaps 1;
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Qy     1 ATGTCATGGTTTAGTGGCCTTCCTCTGTCCCTAAAGTGGATGAACGAAAACAGCCTGGGGT   60
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Qy   181 CCTCCGGTGCCCCTGCAGGATGACGCCTTCATCCGGAGGGCCTGGAGGGCAAGGGCAG    240
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Db  2735 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCCACCCTGATGCTTGGGATC 2794
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Qy  2101 TATGCCAGACATCTTCCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGT    2160
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Db  3275 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCCAATGAGACC    3334

Qy  2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCGTG    2700
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Qy  2701 ATTCTGCTGGTGTTTGCGCTGGCCTGTATCTGCATGTCAGCAGTGGAGTCGACTGCC    2760
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Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGGAGATGAGGAGCTA    2820
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Qy  2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3000
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Qy  3001 GGTGTCGAGTGCCTGCGCGGCTGCTCAACGAGTCATCGCTGACTTTGATGAGATTATCAGC 3060
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Qy  3061 GAGGAGCGCGGTTCCCGGCAGCTGCGAAAAGATCAAGACGATTGGTAGCACCTACACATGGCTGCC 3120
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Qy  3121 TCAGGGGCTGAACGGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGCT 3180
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Qy    781 GTCCTCAGCGGCCGGCCTCTCCACCTTGATCTTGGCCTGGCCAACTTAACCGT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTCCTCAGCGGCCGGCCTCTCCACCTTGATCTTGGCCTGGCCAACTTAACCGT 840

Qy    841 GGTGATGCCTTCCTCTGGAAGCAGTCGGGTGCCAATGTCGGTGCTGCTCCTCGCACCAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGTGATGCCTTCCTCTGGAAAGCAGTCGGGTGCCAATGTCGGTGCTGCTCCTCGCACCAAC 900

Qy    901 GTCATTGGCATCCTGCGACACACTATCCAGCAGAGAGGTGTCTCAGCAGAGTTCAGGAG 960
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RESULT 5
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DEFINITION  Sequence 5 from Patent WO0148164.
ACCESSION   AX189761
VERSION     AX189761.1  GI:15143135
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hammond,H.K. and Gao,M.
  TITLE     Gene therapy for congestive heart failure
  JOURNAL   Patent: WO 0148164-A 5 05-JUL-2001;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
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BASE COUNT      699 a    1025 c    1061 g    764 t
ORIGIN

Query Match             98.1%;  Score 3484.8;  DB 6;  Length 3549;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 3517; Conservative    0; Mismatches   32; Indels    3; Gaps    1;

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Qy     61 GAACGCAATGGGCAGAAGCGGTTCGCGGCCGGTTCGCGGCGTGGCACTCGGGCAGGTGGCTTCTGCACG  120
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Db     2938 ATGTTTGCCTCCAATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCAAACAATGAG  2997

Qy     3001 GGTGTCGAGTGCCTGCGCGTGCTCAACGAGATCATCGCGTGACTTTGATGAGATTATCAGC  3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2998 GGTGTCGAGTGCCTGCGCGTGCTCAACGAGATCATCGCGTGACTTTGATGAGATTATCAGC  3057

Qy     3061 GAGGAGCGGTTCCGGCAGCTGAAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3058 GAGGAGCGGTTCCGGCAGCTGAAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3117

Qy     3121 TCAGGGCTGAACGACCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3118 TCAGGGCTGAACGACCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3177

Qy     3181 GACTACGGCCATGCGGCTCATGGAGCAGATGAGACAATCAATGAGCACTCCTTCAACAAT  3240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3178 GACTACGGCCATGCGGCTCATGGAGCAGATGAGACAATCAATGAGCACTCCTTCAACAAT  3237

Qy     3241 TTCCAGATGAAGATTGGGCTGAACATGGCCCAGTGTCATCGGGGCTCGG  3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3238 TTCCAGATGAAGATTGGGCTGAACATGGCCCAGTGTCATCGGGGCTCGG  3297

Qy     3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAAATGTCTCTAGTCGTATGGACAGCACG  3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3298 AAGCCACAGTATGACATCTGGGGAACACAGTGAAATGTCTCTAGTCGTATGGACAGCACG  3357

Qy     3361 GGGGTCCCGACCGAATCCAGGTGACCCGAGTCAGGTTCTAGCTGCCAAGGGC  3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3358 GGGGTCCCGACCGAATCCAGGTGACCCGAGTCAGGTTCTAGCTGCCAAGGGC  3417

Qy     3421 TACCAGCTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC  3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3418 TACCAGCTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC  3477

Qy     3481 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGACC  3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3478 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGACC  3537

Qy     3541 AAGGTGGCACT 3552
            |||||||||||
Db     3541 AAGGTGGCACT 3549

Qy     601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTAGTGTTGGTCGTGGGGCATCCTGGGGC  660
```

The page consists of a two-sequence nucleotide alignment (query "Qy" vs. database "Db"), arranged in two blocks of aligned rows with flanking position numbers.

Right-hand block:

	Sequence	Start	End
Qy	ATGCCGGCTGGGTTCCTGATCGTGCCTTC...CAGGCCTTCCGC	1741	1800
Db	ATGCCGCGATGGGTTCCTGATCGTGCCTTC...CAGGCCTTCCGC	1738	1797
Qy	CAGATGGGCATTGATGATTCCAGCAAGACAACCGGGGCACCCGAACCCT	1801	1860
Db	CAGATGGGCATTGATGATTCCAGCAAAGAACAACCCGGGCACCCAGAACCCT	1798	1857
Qy	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCGCAGCATTGATCAGCTG	1861	1920
Db	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCGCAGCATTGATCAGCTG	1858	1917
Qy	CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAAG	1921	1980
Db	CGGAAGGACCATGTGCGCCGGTTTTTGCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG	1918	1977
Qy	TACTCCCGGAAGGTGGATCCCCGCTTCGGGAGCCTACGTTGCCGTGCCGTTGGTCTTC	1981	2040
Db	TACTCCCGGAAGGTGGATCCCCGCTTCGGGAGCCTACGTTGCCGTGCCGTTGGTCTTC	1978	2037
Qy	TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCTGATGCTTGGGATC	2041	2100
Db	TGCTTCATCTGCTTCATCCAGCTTCTCAATTTTCCACACTCCACCCTGATGCTTGGGATT	2038	2097
Qy	TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCGATCGTGTCGTGTACTCCTGT	2101	2160
Db	TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTGCGATCGTGTCGTGTACTCCTGT	2098	2157
Qy	GGTTCTCTGTCCCTAAGGCCCGCAACGTCTGTCCCGCGCATTGTCCGCTCACGGGCA	2161	2220
Db	GGTTCTCTGTCCCTAAGGCCCGCAACGTCTGTCCCGCGCATTGTCCGCTCACGGGCA	2158	2217
Qy	CATAGCACCGAGTTGGCATCTTTCCGTCGTTGTTTACTTCTGCCATTGCCAAC	2221	2280
Db	CATAGCACCGAGTTGGCATCTTTCCGTCGTTGTTTACTTCTGCCATTGCCAAC	2218	2277
Qy	ATGTTCACCTGTAACCACACCCCCATACGGAGCGTGTCAGCCCGGATGCTGAATTTAACA	2281	2340
Db	ATGTTCACCTGTAACCACACCCCCATACGGAGCGTGTCAGCCCGGATGCTGAATTTAACA	2278	2337
Qy	CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGGCCTGGATGCT	2341	2400
Db	CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGGCCTGGATGCT	2338	2397
Qy	CCCCTGTGTGAGGGCCACCATGCCCACCTGCCAGCTTTCCTGCACATCAGCAGCATCGGGAACATG	2401	2460
Db	CCCCTGTGTGAGGGCCACCATGCCCACCTGCCAGCTTTCCTGCACATCAGCAGCATCGGGAACATG	2398	2457
Qy	CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCACATCAGCAGCATCGGGAAGTTGGCC	2461	2520
Db	CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCACATCAGCAGCATCGGGAAGTTGGCC	2458	2517
Qy	ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTCTTGGCTCCCCAGCCACC	2521	2580
Db	ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTCTTGGCTCCCCAGCCGCC	2518	2577
Qy	ATCTTTGACAACTATGACTTGCTTGGCGTCCAATCACTCGGGCAACA...CCCTGTG	2581	2640
Db	ATCTTTGACAACTATGACTTGCTTGGCGTCCAATCACTCGGGCAACA...CCCTGTG	2578	2637
Qy	TTTGATGGGCTGGACTGTCCAGCTGCGCGTGGCGCTGTATCCGCAAATATGACCCCTGTG	2641	2700
Db	TTTGATGGGCTGGACTGTCCAGCTGCGCGTGGCGCTGTATCCGCAAATATGACCCCGTGTG	2638	2697
Qy	ATTCTGCTGGTGTTTGGCGCTGCGCTGTATCCGCATGCTCAGCAGGTGGACTGGA	2701	2760
Db	ATCTTTGCTGGTGTTTGGCGCTGCGCTGTATCCGCATGCTCAGCAGGTGGAATCGCC	2698	2757
Qy	CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGGAGAAGGAGGAGCTA	2761	2820
Db	CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGAGGAGGAGCTA	2758	2817

Left-hand block (positions 601–1740 / 598–1737):

	Sequence	Start	End
Db	CATAGCTTCCGCAGGACTCCATGTGGGTGTGGTGAGTAACGTGGTGCTGCTGGGCATCCTGGCC		660
Qy	GCAGTGCAGGTCGGGGGCGCTCTCGCAGCAGACCCGCGAGCCCTCTGCGGGCCTCTGG	661	720
Db	GCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGACCCGCGAGCCCTCTGCGGGCCTCTGG	661	720
Qy	TGCCCTGTGTTCTTTGTCTTGTTTGTCTACAACGGCCTTCCACCTTGCATTTGATCTTGGGCTGGCTGCC	721	780
Db	TGCCCTGTGTTCTTTGTCTTGTTTGTATACATCGGCATACGCGTTTCTTCCACCTTGCATTTGATCTTGGGCTGGCTGCC	721	780
Qy	GTCCCTCAGCGCGGCCTGGGCCTTCTCCACCTTGCATTTGATCTTGGGCCTGGCAACTTAACCGT	781	840
Db	GTCCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGGCCTGGCAACTTAACCGT	781	840
Qy	GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCGTGTCCTGTGCTGCACCAAC	841	900
Db	GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCGTGTCCTGTGCTGCACCAAC	841	900
Qy	GTCATTGGCATCGCACACTATCCAGCAGAGGTGTCTCAGCGCGCCTTTCAGGAG	901	960
Db	GTCATTAGCATCACTATCCAGCAGAGGTGTCTCAGCGCGCCTTTCAGGAG	901	960
Qy	ACCCGCGGGTACATCCAGGCCCGGCTTCCACCTGCAGCATGAGAATCGGCAGCAGGAGGCCGG	961	1020
Db	ACCCGCAGTTACATCCAGGCCCGGCTTCCACCTGCAGCATGAGAATCGGCAGCAGGAGGCGG	961	1020
Qy	CTGCTGCTGTCGCTGGTATTGCCCCAGCAGCGTTGCCCATGCCATGGAGATGAAAGAACATCAACACA	1021	1080
Db	CTGCTGCTGTCGCTGGTATTGCCCCAGCACGTTGCCCATGCCATGGAGATGAAAGAACATCAACACA	1021	1080
Qy	AAAAAAGAAGACATGATGTTCCACAAGATCTTACATACAGAAGAGCATGACAAATGTCAGCATC	1081	1140
Db	AAAAAAGAAGAC---ATGTTCCACAAGATCTTACATACAGAAGAGCATGACAAATGTCAGCATC	1081	1137
Qy	CTGTTTGCAGACCCTGAATGAGCTCTTTTGCCCGGTTGACAAGGCTGCTCGTGTGTCAGGGCTGTGCTGCGGAAATCACTGC	1141	1200
Db	CGTTTTGCAGACACCCTGAATGAGCTCTTTTGCCCGGTTGACAAGGCTGGCTGCTCGTGTGTCAGGGCTGTGCTGCGGAGAAATCACTGC	1138	1197
Qy	GTCATGACCCCTGAATGAGCTCTTTTGCCCGGTTTGACAAGGCTGGCTGCGGGTGGGCGCGTG	1201	1260
Db	GTCATGACCCCTGAATGAGCTCTTTTGCCCGGTTTGACAAGGCTGGCTGCGGGTGGGCGCGTG	1198	1257
Qy	CTGAGGATCAAGATCTTGGGGGACTGTGTTACTACTGTGTCAGGGGCTGCCCGGAGGGCCCGG	1261	1320
Db	CTGAGGATCAAGATCTTGGGGGACTGTGTTACTACTGTGTCAGGGGCTGCCCGGAGGGCCCGG	1258	1317
Qy	GCCGACCATGCCCACTGCTGTGTGGAAATGGGGTAGAACATGATTGAGGGCATCCACAGCGGCGGCCGTG	1321	1380
Db	GCCGACCATGCCCACTGCTGTGTGGAAATGGGGTAGAACATGATTGAGGGCATCCACAGCGGCGGCCGTG	1318	1377
Qy	GTACGTGAGGTGACAGGTGTGAAATGTGAAACATGCGCGTGGGCGTGGGCCGCGTG	1381	1440
Db	GTACGTGAGGTGACAGGTGTGAAATGTGAAACATGCGCGTGGGCGTGGGCCGCGTG	1378	1437
Qy	CACTGCGCGCGTCCTTGGCTTGGCAGTTGCGGAAATGGCCAGTTCGATGTGTTGTCCAATGATGTGACC	1441	1500
Db	CACTGCGCGCGTCCTTGGCTTGGCAGTTGCGGAAATGGCCAGTTCGATGTGTTGTCCAATGATGTGACC	1438	1497
Qy	CTGGCCAACCACCACATGAGGAGGCCGGGCATCCACAATCACTCGGGCAACA	1501	1560
Db	CTGGCCAACCACCACATGAGGAGGACGGGCATCCACAATCACTCGGGCAACA	1498	1557
Qy	CTGCTCAAGGAGCAGCAGCATTGAGACTTTTTCCTCATCCTGTGGTCGGAGGCGCAACGCGG	1561	1620
Db	CTGCTCAAGGAGCAGCAGCATTGAGACTTTTTCCTCATCCTGTGGTCGGAGGCGCAACGCGG	1558	1617
Qy	TACCTCAAGGACCAGCAGCACATTGAGACTTTCCTCATCCTGTGAAAACCGAAA	1621	1680
Db	TACCTCAAGGACCAGCAGCACATTGAGACTTTCCTCATCCTGTGAAAACCGAAA	1618	1677
Qy	GAGGAGAAGGCCATGTCTGGCCAAGCTGCAGCCGACTCGGGCGACTCCATGGAAGGGCTG	1681	1740
Db	GAGGAGAAAGCCATGTCTGGCCAAGCTGCAGCCGACTCGGGCGACTCCATGGAAGGGCTG	1678	1737

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                              /note="Modified AC-VI"
BASE COUNT      703 a   1036 c   1067 g    776 t
ORIGIN

Query Match        96.9%;   Score 3443.2;   DB 6;   Length 3582;
Best Local Similarity  98.3%;   Pred. No. 0;
Matches 3491;   Conservative  0;   Mismatches  0;   Indels 58;   Gaps 3;   Indels 1;
```

Right block (positions 1–1020):

```
Qy    1 ATGTCATGGTTAGTGCCTCCTGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22 ATGTCATGGTTAGTGCCTCCTGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   81

Qy   61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGCACTCGGGCAGGTGGCTTCGCACG  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGCACTCGGGCAGGTGGCTTCGCACG  141

Qy  121 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCCCACCCCTGCGGGCCCC  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142 CCCCGCTATATGAGCTGCCTCCGGATGCAGAGCCACCCAGCCCACCCCTGCGGGCCCC  201

Qy  181 CCTCGGTGCCCCTGCAGGATGAGCCGCCTCCCACATCACTGCCCTGGCT          240
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  202 CCTCGGTGCCCCTGCAGGATGAGCCGCCTCCCACATCACTGCCCTGGCT          261

Qy  241 GAGCTGGGGCGCTGCGGGCAGTGGCCCGACGCGGCCCGACGAGTGGCGATCCTGTGGCGC  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  262 GAGCTGGGGCGCTGCGGGCAGTGGCCCGACGCGGCCCGACGAGTGGCGATCCTGTGGCGC  321

Qy  301 GGGGGACGGTGAGGTGGCGCCGACCGGCCCGAAGCAGTCCGTTCGGTTCCGTTCGCGGCGGCTCGG  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  322 GGGGGACGGTGAGGTGGCGCCGACCGGCCCGAAGCAGTCCGTTCGGTTCCGTTCGCGGCGGCTCGG  381

Qy  361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGTTCCGTGTATGGACAGCAGACG  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  382 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGTTCCGTGTATGGACAGCAGACG  441

Qy  421 CAGCGGTACTTCTTCCGAGATGAACCAGCAGGACCAGAGGTTCTAGCTGCCCAAGGGC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  442 CAGCGGTACTTCTTCCGAGATGAACCAGCAGGACCAGAGGTTCTAGCTGCCCAAGGGC  501

Qy  481 CTGCTCACGCGGTGCTGCTGGTTTCCACGCGCCGCCCGCCTCCAGCCTGCCTAT      540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  502 CTGCTCACGCGGTGCTGCTGGTTTCCACGCGCCGCCCGCCTCCAGCCTGCCTAT      561

Qy  541 GTGGCACTGTTGGCCGTGTGCCGCCGTGTTCGTGTGGGGCTCATGGTGGTGTGTAACCGG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  562 GTGGCACTGTTGGCCGTGTGCCGCCGTGTTCGTGTGGGGCTCATGGTGGTGTGTAACCGG  621

Qy  601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTACGTGGTGCTCGGGCATCCTGGGC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  622 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTACGTGGTGCTCGGGCATCCTGGCG  681

Qy  661 GCAGTGCAGGTCGGGGCGTCGGGGGCGCCTCTCGCAGCAGACCCGGCGAGCCCCTCTGG  720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  682 GCAGTGCAGGTCGGGGCGTCGGGGGCGCCTCTCGCAGCAGACCCGGCGAGCCCCTCTGG  741

Qy  721 TGCCCTGTGTTCTTTGTCTACATCGCTGGCCTACACGGTCGTCCCCATCCGCAGCGGGCTGCC  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  742 TGCCCTGTGTTCTTTGTCTACATCGCTGGCCTACACGGTCGTCCCCATCCGCAGCGGGCTGCC  801

Qy  781 GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCAACTTAACCGT  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  802 GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCAACTTAACCGT  861

Qy  841 GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTCCTCTGCACCAAC  900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  862 GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTCCTCTGCACCAAC  921

Qy  901 GTCATTGGCATCTGCACACACTATCCAGGAGAGTGTCTCCAGAGAGTGCTTTCAGAG  960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  922 GTCATTGGCATCTGCACACACTATCCAGGAGAGTGTCTCCAGAGAGTGCTTTCAGGAG  981

Qy  961 ACCCGGCGGTTACATCCAGCCCCCACCTGCAGCATGAGAATCGGCAGGAGCGCG     1020
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Left block (positions 2818–3549):

```
Qy 2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGCGGCCCACTTC 2880
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2818 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGCGGCCCACTTC 2877

Qy 2881 CTTGCCCCGGAGGCGCCAATGATGAACTCTACTATCAGTCGTGTGGCTGTGGCTGTT 2940
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2878 CTGGCCCCGGAGGCGCCAATGATGAACTCTACTATCAGTCGTGTGGCTGTGGCTGTT 2937

Qy 2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGCCAAACAATGAG 3000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2938 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 2997

Qy 3001 GGTGTGTCGAGTGCCGCTGCGGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2998 GGTGCCAGTGCCGCTGCGGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057

Qy 3061 GAGGAGCGGTTCCGGGCCAGCTGGGAAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3058 GAGGAGCGGTTCCGGGCCAGCTGGGAAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3117

Qy 3121 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGCCGCTCCCACATCACTGCCCCTGGCT 3180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3118 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGCCGCTCCCACATCACTGCCCCTGGCT 3177

Qy 3181 GACTACGGCCATGCGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3178 GACTACGGCCATGCGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3237

Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGCAGTGTCATCGGGGCTCGG 3300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGCAGTGTCATCGGGGCTCGG 3297

Qy 3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGACG 3360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3298 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGACG 3357

Qy 3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3358 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCCTGTACCAGGTTCTAGCTGCCAAGGGC 3417

Qy 3421 TACCAGTGGAGTGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGAGATGACCACCTAC 3480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3418 TACCAGTGGAGTGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGAGATGACCACCTAC 3477

Qy 3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGAGACC 3540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3478 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGAGACC 3537

Qy 3541 AAGGTGGGCACT                                              3552
        ||||||||||||
Db 3538 AAGGTGGGCACT                                              3549
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Db   982 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACCCCGGGTTACATCCAGGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1041

Qy  1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1101

Qy  1081 AAAAAAGAGAAGACATGATGTTCCACAAGATCTTCACATACACGAAGCATGACAATGTCAGCATC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102 AAAAAAGAGAAGACATGATGTTCCACAAGATCTTCACATACACGAAGCATGACAATGTCAGCATC 1161

Qy  1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGCCAGTCCCAGTGCACTGCGCAGGAGCTG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1162 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGCCAGTCCCAGTGCACTGCGCAGGAGCTG 1221

Qy  1201 GTCATGACCCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1222 GTCATGACCCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGT 1281

Qy  1261 CTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1282 CTGAGGATCAAGATCTTAGGAGACTGTACTACTGCGTGTCAGGGCTGCCCGAGGCCCGG 1341

Qy  1321 GCCGACCATGCCCACTGCTGTGTGTGAGATGGGGTAGACATGATTGAGGGCCATCTCGCTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1342 GCAGATCACCGCCCACTGCTGTGTGTGAGATGGGGTAGACATGATCGAAGCCATCTCGCTG 1401

Qy  1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCATCCACAGCGGGCGCGTG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1402 GTGCGTGAGGTAACAGGTGTGAACATGCGCGTGGCATCCACAGCGGCGACGTGTG 1461

Qy  1441 CACTCGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC 1500
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1462 CATTGCGGCGTCCTTGGCCTACGCAGGTTTGATGTCTGGTCAAACGATGTGACC 1521

Qy  1501 CTGGCCAACCACCATGAGGACGCAGGACGCCGGGGGCT---GGCCGGCGCATCCACATCACTCGGGCAACA 1560
         ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db  1522 CTGGGCTAACCACACATGAGGACGCCGGGGGGC---GGCCGGCGCATCCACATCACTCGGGCTACA 1578

Qy  1561 CTGCAGTACTTGAACGGGGACTACAGCGGTGGAGCGGGACCTGGTGGGCGCAACGCG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1579 CTGCAGTACTTGAACGGGGACTATAGCGGGTGGAGCGGGACCTGGTGGGTGAACGCAATGCG 1638

Qy  1621 TACCTCAAGGAGCAGCAGCACATTGAGACTTTCCTCATCGTGGGCGCCAGCGCCAGACGGAAA 1680
         ||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||
Db  1639 TACCTCAAGGAGCAGCAGCAGTGCATTGAGACTTTCGCATCTTGGCGCCAGCGCCAGAACGGAAA 1698

Qy  1681 GAGGAGAAGGCCATGCTGGCCAAGTCGCAGCGAGACTCGGGGACTCCATGGAAGGGCTG 1740
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Db  1699 GAGGAGAAAGCCATGCTGGCCAAGTCGCAGCGAGACACAGGGGACTCCATGGAAGGGACTG 1758

Qy  1741 ATGCCCGCGCTGGGTTCCTGATCGTCGCCTTCTCCCGGGACCAAGGACTTCCAGGGCCTTCCGC 1800
         ||||||||||||||||||||||||| |||| |||||||||||||||||||||||||||||
Db  1759 ATGCCCGCGTGGGTTCCTGACCGTCGCCTTCTCCGGGACCAAGGACTTCTAAGGCATTCCGC 1818

Qy  1801 CAGATGGGCATTGATGATTCTAGCAAAGACAACCCGGGGCACCCGGCACCCTGAACCCT 1860
         ||||||||||||||||||||| |||| ||||||||||||||||||||||||||
Db  1819 CAGATGGGCATTGATGATTCTAGCAAAGACAACCGGGGGTGCCCAAGATGCTCTGAACCCT 1878

Qy  1861 GAGGATGAGGGTGGATGAGTTCCTGAGGCCGCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1879 GAAGATGAGGGTGGATGAGTTCCTGAGGCCGCGTGCCATCGATGCCCGCAGCATTGATCAGCTG 1938

Qy  1921 CGGAAGGACCATGTGCCCGGTTTCTGCTCACCTTCAGAGAGATGCTTGAGAAGAAG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1939 CGGAAGGACCATGTGCCCGGTTTCTGCTCACCTTCCAGAGAGAGAGATGCTTGAGAAGAAG 1998

Qy  1981 TACTCCCGGAAGGTGAATCCCCGCTTCGGAGCCTACGTTGCCTGTTGGTCTTC 2040
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Db  1999 TACTCCCGGAAGGTGAATCCCCGCTTCGGAGCCTACGTTGCCTGTTGCCTGTTCTTC 2058

Qy  2041 TGCTTCATCTGCTTCATCCAGCTTCTCTGCTCTGTCATCTTCCCACACTCCACCCTGATGCTGTTGGGATC 2100
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Db  2059 TGCTTCATCTGCTTCATCCAGCTTCTCTGCTCTGTCATCTTCCCACACTCCACCCTGATGCTGTTGGGATC 2118

Qy  2101 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTCGTCGTGATCGTGTGTACTCCTGT 2160
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Db  2119 TATGCCAGCATCTTCCTGCTGCTGCTAATCACCGTCGTCGTGATCGTGTGTACTCCTGT 2178

Qy  2161 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCGTCACGGGCA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2179 GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCGTCACGGGCA 2238

Qy  2221 CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTGTGTTACTTCTGCCATTGCCAAC 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2239 CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTGTGTTTACTTCTGCCATTGCCAAC 2298

Qy  2281 ATGTTCACCTGTAACCACACCCCATACACCCCATACGGAGCTGTGTCGAGCCCGGATGCTGAATTTAACA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2299 ATGTTCACCTGTAACCACACCCCATACACCCCATACGGAGCTGTGTCGAGCCCGGATGCTGAATTTAACA 2358

Qy  2341 CCTGCTGACATCACTGCCTGCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2359 CCTGCTGACATCACTGCCTGCACCTGCAGCAGCTCAATTACTCTCTCGGGCCTGGATGCT 2418

Qy  2401 CCCCTGTGTGAGGGCACCATGCCCAACTGCAGCTTTCCTGAGTACTTCATCGGGAACATG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2419 CCCCTGTGTGAGGGCACCATGCCCAACTGCAGCTTTCCTGAGTACTTCATCGGGAACATG 2478

Qy  2461 CTGCTGAGTCTCTTGGCCAGCTGCTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
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Db  2479 CTGCTGAGTCTCTTGGCCAGCTGCTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2538

Qy  2521 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGCTGCTCTGCTCTTGGCTTGGCTTCTTCCAATGAGACC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2539 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGCTGCTCTGCTCTTGGCTTGGCTTCTTCCAATGAGACC 2598

Qy  2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCTGCAGCTGCGAGGAGGGTGGCCCTCAAATATGACCCCGTG 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2599 ATCTTTGACAACTATGACCTACTGCTTGGCGTCTGCAGCTGCGAGGAGGGTGGCCCTCAAATATATAGACCCCGTG 2658

Qy  2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGGTGGCCCTCAAATATGACCCCGTG 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2659 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGGTGGCCCTCAAATATATAGACCCCGTG 2718

Qy  2701 ATTCTGCTGGTGTTTGCGCTGGCGTGTATCGCATGCGCAGTGGAGTGCTCAGCGACTGCC 2760
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Db  2719 ATTCTGCTGGTGTTTGCGCTGGCGTGTATCGCATGCGCAGTGGAGTGCTCAGCGACTGCC 2778

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGGATGGAGGAGCTA 2820
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Db  2779 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGGATGGAGGAGCTA 2838

Qy  2821 CAGGCATACAACCGGAGGCGTCGCTGCATAACATTCTGCCCAAGGACGCGGCCGCCCACTTC 2880
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Db  2839 CAGGCATACAACCGGAGGCGTCGCTGCATAACATTCTGCCCAAGGACGCGGCCGCCCACTTC 2898

Qy  2881 CTGGGCCCGGAGCGCCGCCAATGATGAACTTCTACTATCAGTCGTGTGAGGCTGACTGCGTGTT 2940
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Db  2899 CTGGGCCCGGAGCGCCGCCAATGATGAACTTCTACTATCAGTCGTGTGTGAGGCTGGCTGCGTGTT 2958

Qy  2941 ATGTTTGCCTTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCAAACAATGAG 3000
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Db  2959 ATGTTTGCCTTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGGCAAACAATGAG 3018

Qy  3001 GGTGTGAGTGCCATGGACTTTGATGTCTGCTCAACGACATCTTGAGAAGAAG 3060
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Db  3019 GGTGTGAGTGCCATGGACTTTGATGTCTGCTCAACGACATCTTGAGAAGAAG 3078

Qy  3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3079 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3138

Qy  3121 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCTCCACATCACTGCCCTGGCT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3139 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCTCCACATCACTGCCCTGGCT 3198
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Qy    601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTACGGTGGTGCTGGGCATCCTGGGCG  660
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Db    737 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTACGGTGGTGCTGGGCATCCTGGGCG  796

Qy    661 GCAGTGCAGGTCGGGGGCGCTCGCAGCAGACCCGCAGACCCGCAGCCCCTGCGGGCCTCTGG  720
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Qy    721 TGCCCTGTGTTCTTTGTCTACATCGGCCTACACGCTCTCCCCATCGGCATGCGGGCTGCC  780
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Db    857 TGCCCTGTGTTCTTTGTCTACATCGGCCTACACGCTCTCCCCATCGGCATGCGGGCTGCC  916

Qy    781 GTCCTCAGCCGCCTGGGCCTTCCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT  840
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Qy    841 GGTGATGCCTTCCTCTGGAAGCAGCAGCTCGGTGCCAATGTGCTGCTTCCTCGCACCAAC  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 GGTGATGCCTTCCTCTGGAAGCAGCAGCTCGGTGCCAATGTGCTGCTTCCTCGCACCAAC  1036

Qy    901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCTTTCAGGAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCTTTCAGGAG  1096

Qy    961 ACCCGCGGTTACATCCAGGCGCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097 ACCCGCGGTTACATCCAGGCGCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG  1156

Qy   1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGGAGATGAAAAGAACATCAACACA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGGAGATGAAAAGAACATCAACACA  1216

Qy   1081 AAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC  1140
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Db   1217 AAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC  1276

Qy   1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGGATCCTGGACTCGCATCGCGCGCAGAGCTG  1200
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Db   1277 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGGATCCTGGACTCGCATCGCGCGCAGAGCTG  1336

Qy   1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGCAAGCTGGCTGCGGAGAATCACTGC  1260
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Db   1337 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGCAAGCTGGCTGCGGAGAATCACTGC  1396

Qy   1261 CTGAGGATCAAGAGTCTTGGGGGACTGTTACTGTGTGTCAGGGCTGCCGGAGGCCCGG  1320
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Db   1397 CTGAGGATCAAGAGTCTTGGGGGACTGTTACTGTGTGTCAGGGCTGCCGGAGGCCCGG  1456

Qy   1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG  1380
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Db   1457 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG  1516

Qy   1381 GTACGTGAGGTGACAGGTGAATGTGAACATGGCAGTTCGATGTGTGTTCCAATGATGTGACC  1440
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Db   1517 GTACGTGAGGTGACAGGTGAATGTGAACATGGCAGTTCGATGTGTGTTCCAATGATGTGACC  1576

Qy   1441 CACTGCGGCGTCCTTGGCTTGGCTGCGGAGGCAGGAGGCCGTGGCCGGCGCGCACGCG  1500
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Qy   1501 CTGGCCAACCACCATGAGGCAGGGGACTACGACGGGGCGCTGGGAGGGCGCAACA  1560
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Qy   1561 CTGCAGCAGTACCTGACAACGGGGGGGCTACGACGGGGCGCTGTGGAGGCGCAACGCG  1620
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Db   1697 CTGCAGCAGTACCTGACAACGGGGGGGCTACGACGGGGCGCTGTGGAGGCGCAACGCG  1756

Qy   1621 TACCTCAAGGAGCAGCAGCACATTGAGACTTTGAGACTTTGAGACGCACAAACGGAAA  1680
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Db   1757 TACCTCAAGGAGCAGCAGCACATTGAGACTTTGAGACTTTGAGACGCACAAACGGAAA  1816
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Qy   1681 GAGGAGAAGGCCATGCTGGCCAAGCTGCAGCGGACTCGGGCGGACTCCATGAAGGGCTG  1740
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Db   1817 GAGGAGAAGGCCATGCTGGCCAAGCTGCAGCGGACTCGGGCGGACTCCATGAAGGGCTG  1876

Qy   1741 ATGCCCGCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTCCAAGGCCTTCCGC  1800
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Db   1877 ATGCCCGCTGGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCCTTCCGC  1936

Qy   1801 CAGATGGGCATTGATGATTCCAGCAAAGACAACACGGGCACCCAAGATGCCCTGAACCCT  1860
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Db   1937 CAGATGGGCATTGATGATTCCAGCAAAGACAACACGGGCACCCAAGATGCCCTGAACCCT  1996

Qy   1861 GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG  1920
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Qy   1921 CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAAG  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2057 CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAAG  2116

Qy   1981 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCGTGTTGGTCTTC  2040
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Db   2117 TACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCGTGTTGGTCTTC  2176

Qy   2041 TGCTTCATCTGCTTCTGCTGCTGCTCTCATCTTCCCACACTCCACCTGATGCTTGGGATC  2100
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Qy   2101 TATGCCAGCATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTGTGTGTACTCCTGT  2160
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Db   2237 TATGCCAGCATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTGTGTGTACTCCTGT  2296

Qy   2161 GGTTCTCGTTCCCTAAGGCCCTGCAACGTCGTGCCCGCAAGTGTCCGCTCACGGGCA  2220
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Db   2297 GGTTCTCGTTCCCTAAGGCCCTGCAACGTCGTGCCCGCAAGTGTCCGCTCACGGGCA  2356

Qy   2221 CATAGCACCGGAGTTGGCATCTTTCCGGCATCCTTGTTTACTTCTGCCATTGCCAAC  2280
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Db   2357 CATAGCACCGGAGTTGGCATCTTTCCGGCATCCTTGTTTACTTCTGCCATTGCCAAC  2416

Qy   2281 ATGTTCACCTGTAACCACACCACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA  2340
          ||||
Db   2417 AT-  2418

Qy   2341 CCTGCTGACATCCACTGCCTGCCACCTGACCAGCTCAATTACTCTCTGGCGCTGGATGCT  2400
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Db   2419 ---  2418

Qy   2401 CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG  2460
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Db   2419 ---GTACTTCATCGGGAACATG  2437

Qy   2461 CTGCTGAGTCTCTTCCTGGCCAGCTCGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
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Db   2438 CTGCTGAGTCTCTTCCTGGCCAGCTCGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2497

Qy   2521 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGCTGCTTCGTCTCGCGGTCCCCCAGCCACC  2580
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Db   2498 ATGATCTTTGTCTTGGGGCTCATCTATTTGTGCTGCTTCGTCTCGCGGTCCCCCAGCCACC  2557

Qy   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTTCCAATGCTTGGCGTTCTTCCAATGAGACC  2640
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Db   2558 ATCTTTGACAACTATGACCTACTGCTTGGCGTTCCAATGCTTGGCGTTCTTCCAATGAGACC  2617

Qy   2641 TTTGATGGGCTGGACTGTGTCGACTGTGCCAGCTGCAGGGAGGGTGCCCTCAAATATAGACCCCTGTG  2700
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Qy   2701 ATTCTGCTGGGTGTTTGCTGGCTGTATCCTGCGCTGCATGGCTGTATCCTGCAGGTGGACTGCC  2760
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Db   2678 ATTCTGCTGGGTGTTTGCTGGCTGTATCCTGCGCTGCATGGCTGTATCCTGCAGGTGGACTGCC  2737

Qy   2761 CGCCTAGACTTCCTCTGGAAACTACACAGGCAACAGAGGGAGGAGGAGAGGAGGAGCTA  2820
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Db             2737
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JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
MEDLINE   92409599
PUBMED   1528892
COMMENT   Original source text: Canis familiaris cardiac muscle cDNA to mRNA.
FEATURES   Location/Qualifiers
     source   1..4046
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /tissue_type="cardiac muscle"
BASE COUNT   743 a   1206 c   1254 g   843 t
ORIGIN

Query Match   86.1%;   Score 3057.6; DB 4; Length 4046;
Best Local Similarity 91.9%;   Pred. No. 0;
Matches 3264; Conservative 0; Mismatches 279; Indels 9; Gaps . 3;

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Qy     1 ATGTCATGGTTAGTGGCTCCTGTCCCTAAAGTGGATGAACGGAAAACAGCGTGGGGT    60
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Db   131 ATGTCGTGGTTTAGTGGCCTCCTGTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT   190

Qy    61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGCAGGTGGCACTCGGCGCCGGGGTGGCTTCTGCACG   120
           |||||||||||| ||||||||      |||||||||||||||          ||||||||||||||||||
Db   191 GAACGCAATGGGCAGAAGCGGT---CCACGGCGCGGGACTTCGGACCAGTGGCTTCTGCACG   247

Qy   121 CCCGCTATATGAGCTGCCTCCGGGATGAGAGCCACCAGCCCCACCCCTGCGGGCCCC   180
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Db   248 CCCCGCTATATGAGCTGCCTCCGGGATGAGAGCCAGCCCCAGTCCCACCCCTGCGGGCTCCC   307

Qy   181 CCTCGGTGCCCCTGGCAGGATGACGCCTCATCCGGAGGGGCGGGCCCAGGCAAG   240
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Qy   241 GAGCTGGGGCTGCGGGGCGGGTGCGCCGAGGTGCCCGATCCGGGCGATCCTGCTGCGGCGC   300
           ||||||||||||||||||||||||||||||||       ||| |||||| ||||||||||||
Db   368 GAGCTGGGGCTGCGGGGCGGGTGCGCCGAGGTG---CCATGTCAGCGGATCCTGCTGCGGCGC   424

Qy   301 GGCGGGACGGCTGAGGTGCGCGCCCAGACGCGGCCCGATCCGTGCGGCGGC   360
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Db   425 GTTGGGGCAGCTGAGGTGCGCCCCTGACCCCCGGGAGTGGCGATCCTGCTGCGGC   484

Qy   361 CGTCGGTGCCAGGTGTTCCAGTGCAGAGTTCCGTTCGGCCGCTGTAC   420
           |||||||||||||||||||||||||||||||| ||||||||||||||||
Db   485 CGTCGGTGCCAGGTGTTCCAGTGCAGAGTTCCGCTCGGCCGCTGTAC   544

Qy   421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCACCGGGTGGTG   480
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Db   545 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCACCGGGTGGTG   604

Qy   481 CTGCTTCACAGCGGTGCTGCTGGCTTCACAGCCGCGCCCCTGCCTAT   540
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Db   605 CTGCTGACAGCGGTGCTGCTGCAGCCTTCATGCTGCGCCCCTGCCTAC   664

Qy   541 GTGGCACTCGTGGCCTGTCGCCGTGCCGCGCCACCCTTCGTGCTGGGGCTCATGGTGTCTCGGGG   600
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Qy   601 CATAGTTCCGCACCAGGACTCCATGTGGGTGGTGAGTTACGTGTCTCGGGATCCTGGGCG   660
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Db   725 CACAGCTTCGCACCAGGACTCCATGTGGGTGGTGGTGTCTACGTGTCTCGGTGGGATCCTGGGCGGCA   784

Qy   661 GCAGTGCAGGTCGGGGGGCGCTCTGCAGCAGACCCGCAGCCCCTCTGCGGGCCTCGG   720
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Qy   721 TGCCCGGTCTTCTTGTCTACATCGCCATGCTTACACGGCTCCTCCCCCATCCGCAATGGGGCTGCC   780
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Db   845 TGCCCGTGTTTTTTGTCTACATCACCACCACGCTCCTCCCCACCACGGCTCCGCATGGGGCAGCT   904

Qy   781 GTCCTCAGCGGCCTGGCCCTCCACCTTGCATTTGATCTTGGCCTGCAACTTAACCGT   840
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Db  2738 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGCAGGGGAGGAGGAGATGGCGGCCACTTC   2797
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCACTTC   2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2798 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCACTTC   2857

Qy  2881 CTGGCCCCGGAGGCCGCCAATGATGAACGGCCGCAATGATGAGTCGTGTGAGTGTGCTGTT   2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2858 CTGGCCCCGGAGGCCGCCAATGATGAACTTCTACTATCAGTCGTGTGAGTGTGCTGTT   2917

Qy  2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG   3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2918 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG   2977

Qy  3001 GGTGTCGAGTGCCTGCCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC   3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2978 GGTGTCGAGTGCCTGCCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC   3037

Qy  3061 GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGAGCGATTGGTAGCACATGGCTGCC   3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3038 GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGAGCGATTGGTAGCACATGGCTGCC   3097

Qy  3121 TCAGGGCTGAACGGCAGCACCTACGATCAGGTGGCCGCTCCCACATCACTGCCCTGGCT   3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3098 TCAGGGCTGAACGGCAGCACCTACGATCAGGTGGCCGCTCCCACATCACTGCCCTGGCT   3157

Qy  3181 GACTACGCCATGGCTCATGGAGCAGCGAGATGAAGCACATCAATGAGCACTCCTTCAAACAAT   3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3158 GACTACGCCATGGCTCATGGAGCAGCGAGATGAAGCACATCAATGAGCACTCCTTCAAACAAT   3217

Qy  3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGCTGTGCAGTGTCATCGGGGCTCGG   3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3218 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGCTGCGCAGTGTCATCGGGGCTCGG   3277

Qy  3301 AAGCCACAGTATGACATCTCGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG   3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3278 AAGCCACAGTATGACATCTCGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG   3337

Qy  3361 GGGGTCCCCGACCGAATCCAGGTGACCGGAATCCAGGTTCTAGCTGCCAAGGGC   3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3338 GGGGTCCCCGACCGAATCCAGGTGACCGGAATCCAGGTTCTAGCTGCCAAGGGC   3397

Qy  3421 TACCAGTCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC   3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3398 TACCAGTCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC   3457

Qy  3481 TTTCTCAATGGGGGCGCCCAGCAGTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC   3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3458 TTTCTCAATGGGGGCGCCCAGCAGTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC   3517

Qy  3541 AAGGTGGGCACT   3552
           |||||||||| |
Db  3518 AAGGTGGGCATT   3529
```

RESULT 8
DOGADENCYC
LOCUS   DOGADENCYC   4046 bp   mRNA   linear   MAM 27-APR-1993
DEFINITION Canis familiaris adenylyl cyclase type VI mRNA sequence.
ACCESSION   M94968
VERSION   M94968.1 GI:163896
KEYWORDS   adenylyl cyclase type VI.
SOURCE   Canis familiaris (dog)
  ORGANISM Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 4046)
  AUTHORS   Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J.,
            Homcy,C.J. and Ishikawa,Y.
  TITLE   Cloning and characterization of a sixth adenylyl cyclase isoform:
            types V and VI constitute a subgroup within the mammalian adenylyl
            cyclase family

The page contains a two-part DNA sequence alignment (query "Qy" vs database "Db"), with each aligned row flanked by position numbers.

Left column alignment (positions ~841–2041):

```
Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCCTCTGCCACCAAC 900
         |||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   965 GGTGACGCCTTCCTCTGGAAGCAGCTCGGTGCCAACATGCTGCTTCCTCTGCCACCAAC 1024

Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCCGCCAGGCCTTTCAGGAG 960
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  1025 GTCATTGGCATCTGCACACTACCCAGCTGAGGTCTCTCAGCCGCCAGGCCTTTCAGGAG 1084

Qy   961 ACCCGGCGGTTACATCCAGGGCCGGCTCCACCTGCAGCATGGAAATCGGCAGCAGGACGG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1085 ACCCGGCGGTTACATTCAGGGCCGGCTGCACCTGCAGCATGGAGATGAGGAACCGGCAGCAGGAACGG 1144

Qy  1021 CTGCTCGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  1145 CTGCTGCTCGGTCCGTGTTGCCCCAGCAGTGTTGCCATGGAGATGAAAGAAGATATCAACACA 1204

Qy  1081 AAAAAGAGACATCTGCACAAGATCTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1205 AAGAAAGAAGACATGATGTTCCACAAGATCTACAATCCAGAAGCATGACAATGTCAGCATC 1264

Qy  1141 CTGTTTGCAGACATTGAGGGGTTCACCCAGCTGCGATCCCAGTGCACTGCGCAGGAGCTG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1265 CTGTTTGCAGACATTGAAGGCTTCACCCAGCTGCGTCCCAGTGCACTGCGCAGGAGCTG 1324

Qy  1201 GTCATGACCCTGAATCAGCTCTTTGCCCGGTTTGACAAGCTGGCTCGCGGAGAATCACTGC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1325 GTCATGACCCTGAACGAGCTCTTCGCCCGGTTTGACAAGCTGGCTCGCGGGAAAATCACTGC 1384

Qy  1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTTCAGGGCTGCCCGGAGGCCCGG 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1385 CTGAGGATCAAGATCTTAGGGGACTGTTACTACTGTGTCGGGGCTGCCCGGAGGCCCGG 1444

Qy  1321 GCCGACCACCATGCCCACTCGTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
         |||||||||||||||||||||||||||| -   |||||||||||||||||||||||
Db  1445 GCAGACCACCATGCCCACTCGTGTGTGGAGATGGGGTTGGACATGATCGAGGCCATCTCGCTG 1504

Qy  1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGGCATCCACAGCGGCGCGTG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1505 GTGCGTGAGGTGACAGGTGTGAACGTGTGGAACATGCGCGTGGGGCATCCACAGCGGCGCGTGTG 1564

Qy  1441 CACTCGCGGCGTCCTTGGCTTCGCGAAATGGCAGTTGCATGTGTGTGACCATGATGTGACC 1500
         |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  1565 CACTCGGTGTCCTTCGGCTTCTCGGCGAAATGGCAGTTCGACGTGTGGTCCAATGACGTGACT 1624

Qy  1501 CTGGCCAACCACCACCACCATGGAGGCAGAGGAGCGGCCTGGCCGCTGGCACTACTCGGGGCAACA 1560
         ||||||||||||||||||||||  -  |||||||||||||| |||
Db  1625 CTGGGCCAACCAACCATATGGAGGC---GGCCCGGGCCGGCCGCATCCACCCGGGCCCACG 1681

Qy  1561 CTTGCAGTACCTGGAACGGGGGACTACGAGGTGGAGCAGCCCGGTGGTGGGCGAGCGCAACGCG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1682 CTGCAGTACCTGGAACGGGGACTACGAGGTGGAGCAGCCCGGTGGTGGGCGAGCGCGGAACGCG 1741

Qy  1621 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTCTCGGCGGACTTTCCTCATCCTCTCGGCGGCCAAACGGAAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||| -  |||
Db  1742 TACCTCGGTGTCGTTTGGCTTGCCCCTGGGCGCGTGTATCTCGCACGCGGCCCCCAGCCAGAAACGGAAA 1801

Qy  1681 GAGGAGGAAGGGCATGTGGGCCAAGCTGCGCAGCGGGACCTGGGCGCCAACTCCATGGAAAGGGGCTG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1802 GAGGAGGAGGAAGGGGCCATGTGGGCCAAGCTGCGCAGCGGGACCTGGGCGCCAACTCCATGGAAGGGCCTG 1861

Qy  1741 ATGCCCGCGCTGGGGTTCGATCGTGGGCTTCCCGACGGACTTCCGGGC 1800
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1862 ATGCCACGCGCTGGGGTGGCGACCGACCGGACTCCCGAGGACTTTCCGC 1921

Qy  1801 CAGATTGGGCATTGATGATTCAGCAAAGACAAACCGGGCACCCAAGATGCCCGAACCCT 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1922 CAGATTGGGCATTGATGATTCAGCAAAGCAACCGGGGTGCCCCAAGATGCCCGAACCCC 1981

Qy  1861 GAGGATGAGGTGGATGAGTTCCTGCGACCGGTTCCTGCGACCGGCCGCATCGATCGATCAGCTG 1920
         |||||||||||||||||||||| -  ||||||||||||||||||||||||||||||||
Db  1982 GAGGATGAGGTCGATGAGTTCCTGGGGCCGGTCCTGCGACCGGCCGCATCGATCAGCTA 2041

Qy  1921 GGTGTCGAGTGCCTGCCGGTTTCTGCTCACCTTCGCCACCTTCGCCACCTTCCAGAGAGAGGATCTTCACGAGAAGAG 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Right column alignment (positions ~1981–3121):

```
Db  2042 CGGAAGGACCATGTGCGCGCCGTTCCTGCTCACCTTCCAGAGGAGGAGGATCTTGAAAAGAAG 2101

Qy  1981 TACTCCCGGAAGGTGGATCCCCGGCTTCGGAGCCTACGTTGCCGTGCCGTGCTGTTGGTCTTC 2040
         ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2102 TACTCAAGGAAGGTGGACCCCCGGCTTCGGAGCCTACGTGGCCGTGCCGTGCTGTTGGTCTTC 2161

Qy  2041 TGCTTCATCTGCTTCATCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATCGTGGGATC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2162 TGCTTCATCTGCTTATCCAGCTCCTCGTCTTCCCACACTCAACCGTGATGTCTTGGGATC 2221

Qy  2101 TATGCCAGCATCTTCCTGCTGCTCGCTCAATCACCGTGCTGCTGATCTGTGCTGTGTACTCCTGT 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2222 TACGCCAGTATCTTGTGCTGGTGTGCTGTGATCACCGTGCCTGCTGACCTGTGCTGTGTACTCCTGT 2281

Qy  2161 GGTTCTCGTTCCTAAGGCCCTGCAACGTCGTCCCGGAGCATTGTCCGCTCACGGGCA 2220
         |||| ||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Db  2282 GGCTCTCTCTCCCAAGGCCCGGCCTCTTCCCGAGCATCATCGCCCGCTCACGGGCA 2341

Qy  2221 CATAGCACCGAGTTGGCATCTTTCCGTCTGTGTTTACTTCTGCCATTGCCAAC 2280
         |||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  2342 CACAGCACGTGGTTGGCATTTTTCAGTCTGCTCAGTGTTCACCTCTGCCATCGCCAAC 2401

Qy  2281 ATGTTCACCTGTAACCACACACCCCATAGGAGCTGTGCAGCCCGGATGCTGGAATTTAACA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2402 ATGTTCACCTGTAACCACACCACCCCATCCGGACCCGTGCAGCCCGGATGCTGAATGTAACA 2461

Qy  2341 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCGGCGGCCTGGATGCT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2462 CCCGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTATTCTCTCGGGCCTGGATGCT 2521

Qy  2401 CCCCTGTGTGAGGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2522 CCGGCTGTGTGAGGGGCACCGCACCCACCTTGCAGCTTGCCTGAGTACTTCGTTGGGAAACATG 2581

Qy  2461 CTGCTGAGTCGCTCTTGGCCAGGTGTCTGCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2582 CTGCTGAGTCGCTCTTGGCCAGCTCGTTTTCCTGCACATCAGCATCGGGAAGTTGGCC 2641

Qy  2521 ATGATCTTTGTCTTGGGGCGCTTCATCTATTTGGTGCTTCTGCTCTGGGGTCCCCAGCCACC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2642 ATGATCTTTGTCTGGGGCGCTTCATTATTTGGTGCTGCTCTGGGGCCCCCCCAGCACC 2701

Qy  2581 ATCTTTGACAAACTATGACCTACTGCTTGGCCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2702 ATCTTTGACAAACTATGACCTACTGCTTGGCCGTGGTCATTGGCTTGGCTTCTTCCAATGACACC 2761

Qy  2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGGTGGAGCGGGAGGGGTGGCCCTCAAATATGACCCCTGTG 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2762 TTTGATGGGCTGGACTGTCCCAGCTGCCCAGCTGCACTGAAATACATGGCACTGAAATACACCCCTGTG 2821

Qy  2701 ATTCTGCTGGTGTTTGCCCTGGCGCGTGTATCTGCATCATGCTCAGCAGTGGAGTCGACTGCC 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2822 ATTCTGCTGGTGTTTGCCCTGGCGCGTGTATCTGCACGCGCAGCAGTGGAATCAACTGCA 2881

Qy  2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGAAGGGAGATGAGGAGGCTA 2820
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2882 CGTCTCGACTTCCTCTGGAAACTGCAGGCAACTGCAGGGGAGAAGGGAGATGAGGAGGAGCTC 2941

Qy  2821 CAGGGCATACAACCGGAGGCGCCCGCTGCTGCATAACATTCTGCCCAAGGACTCCCACTTC 2880
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2942 CAGGGCCTACAACCGGAGGCGCCCGCTGCTGCATAAACATTCTGCCTAAGGACGCGGCTGGCCCACTTC 3001

Qy  2881 CTGGGCCCGGGAGCGCCCAATGATGATCGCTACTATCAGTCGTGTGAGTCGTGTGGCGTGTT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3002 CTGGGCCCGGGAGCGCCCGGAACGCGCCGCGGTGCCCAGAGTGCTCGTGTGGTGTGGCCGTC 3061

Qy  2941 ATGTTTGCCTCCATTGCCAACTTCTGAGTTCTATGTGGAGCTCGAGGCAAACAATGAG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3062 ATGTTTGCCTCCATTGCCAACTTTTCCAACTTTCTGAGTTCTATGTGGAGCTCGAGGCAAACAATGAG 3121

Qy  3001 GGTGTCGAGTGCCTGCCGGTTTCTGCTCACCTTCAACGAGATCATCGCTGCGACTTTGATGAGATTATCAGC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 9
I29958
LOCUS       I29958                  4046 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5578481.
ACCESSION   I29958
VERSION     I29958.1  GI:1820749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4046)
  AUTHORS   Ishikawa,Y.
  TITLE     Cloning and characterization of a cardiac adenylyl cyclase
  JOURNAL   Patent: US 5578481-A 1 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1..4046
                     /organism="unknown"
BASE COUNT      743 a   1202 c   1257 g    844 t
ORIGIN

Query Match             85.9%;  Score 3051.2;  DB 6;  Length 4046;
Best Local Similarity   91.8%;  Pred. No. 0;
Matches 3260;  Conservative    0;  Mismatches  283;  Indels    9;  Gaps    3;
```

```
Qy          1 ATGTCATCGTTTAGTGGCCTCCTGGTCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        131 ATGTCGTCGTTTAGTGGCCTCCTGGTCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT   190

Qy         61 GAACGCAATGGGCAGAAGCGTTCGCGGCACTCGGCGGTGGCTTCTGCACG   120
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GAACGCAATGGGCAGAAGCGT---CCACGCGCGGGACTCGGACCAGTGGCTTCTGCACG   247

Qy        121 CCCCGCTATATGAGCTGCCTCCGGGATGCCGAGGAGCAGCCCACCCCTGCGGGGGCCCC   180
              |||||||||||||||||||||||| ||||||     |||
Db          1 .
```

(DNA sequence alignment — Qy/Db rows with similarity bars, base positions ranging from 181–1384 on the upper block and 3061–3673 on the lower block)

```
Db   3541 AAGGTGGGCACT 3552
          ||||||||||||
Db   3662 AAGGTGGGCATT 3673
```

Left column:

```
Qy  1261  CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGTGCCGGAGGCCCGG  1320
          ||||||||||||||||||||||||||||||||||| |||||||||| |||||||||||||
Db  1385  CTGAGGATCAAGATCTTAGGGGACTGTTACTACTGTGTGTCGGGGCGCCCGGAGGCCCGG  1444

Qy  1321  GCCGACCACTGCCCACTGCTGGTGTGGGAGATGGGGGTTGACATGATTGAGGGCATCTCGCTG  1380
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1445  GCAGACCATGCCCACTGGTGTGTGGGGACATGATGGGGTGGACATGATCGAGGGCATCTCGCTG  1504

Qy  1381  GTACGTGAGGTGACAGGTGTGAAATGTGAACATGCGCGTGGGCATCCACGCGGGCGCGTG  1440
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  1505  GTGCGTGAGGTGACAGGTGTGAACATGCGCGTGGGCATCCACGCGGGCGGGGCGTGTG  1564

Qy  1441  CACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACC  1500
          |||||| ||||| ||||||||||||||| |||||||||||||||||||||||||||||||
Db  1565  CACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTCGACGTGTGGTCCAATGACGTGACT  1624

Qy  1501  CTGGCCAACCACATGGAGACGGAGGAGGCCGGCATCCAACTCACCGGCGGCAACA  1560
          ||||| |||||||||||||||| |||   ||||| ||||||||| ||||| |||||
Db  1625  CTGGCCAACCACATGGAGAGGC---GGCCCGGCGCCCATCCACATCACCGGCGGCCACG  1681

Qy  1561  CTGCAGTACCTGAACGGGGGACTACAGAGGTGGAGCGCGCCAGGCCCGTGGTGCGCGGCAACGCG  1620
          ||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||||| |||||
Db  1682  CTGCAGTACCTGAACGGGGGACTACAGAGGTGGAGCGCGCCAGGCCCGTGGTGCGCGGCAACGCG  1741

Qy  1621  TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCGCCAGCAGCCCATGGGAAA  1680
          ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db  1742  TACCTCAAGGAGCAGCAGCACATCGAGACCTTCCTCATCCTGGGCGCGCCAGCCGCCCATGGGAAA  1801

Qy  1681  GAGGAGAAGGCCATGCTGGGCCAAGCTGCAGCGGACTCGGGGCCAACTCCATGGAAGGGCTG  1740
          ||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||| |||
Db  1802  GAGGAGAAGGCCATGCTGGGCCAAGCTGCAGCGGACGCGGGGCCAACTCCATGGAAGGCCTG  1861

Qy  1741  ATGCCCGCCTGGGTTCCTGATCGTGCGCTTCCCGGACCCAAGGACTCCAAGGCCTTCCGC  1800
          |||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||
Db  1862  ATGCCCACGCTGGGTGGCCGACCGCGCCTTCCCGGACCCAAGGACTCCAAGGCCTTTCCGC  1921

Qy  1801  CAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCT  1860
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  1922  CAGATGGGCATTGATGATTCCAGCAAAGACAACACGGGGCACCCAAGATGCCCTGAACCCC  1981

Qy  1861  GAGGATGAGGTGGATGAGTTCCTGCCCGGTTCCTGAGCCCGCCGCATTGACATCGATCAGCTG  1920
          ||||||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||||
Db  1982  GAGGATGAGGTGGATGAGTTCCTGCCCGGTTCCTGAGCCCGCCGCATTGACATCGATCAGCTA  2041

Qy  1921  CGGAAGGACCACATGTGCCCGGTTTCTGCTCACTTCGGAGCCTACGTTGCCCGTGTGGTCTTC  1980
          ||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db  2042  CGGAAGGACCACATGTGCCCGGTTTCTGCTCACTTCGGAGCCTACGTTGCCCGTGTGGTCTTC  2101

Qy  1981  TACTCCCGGAAGGTGATCCCGCCTTCGGAGCCTTCGGAGCGCCTGGCCGTGTGCGCGCTGGTCTTC  2040
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Db  2102  TACTCAAGGAAGGTGGACCCCGCTTCGGAGCCTTCGGAGCGCCTGGCCGTGTGCGGCTGGTTCTTC  2161

Qy  2041  TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTTCCACCTTCCAGCTTCTTGGGATC  2100
          ||||||||||||| |||||||||||||||| |||||||||||||||| |||||||||||||||
Db  2162  TGCTTCATCTGCTTTATCCAGCTTTCTCGTCTTCCCACACTTCAACCCTGCTTCAACCGTGATGCTTTGGGATC  2221

Qy  2101  TATGCCAGCATCTTCCTCGCTGCTAATCACGTGCTGTGATCTCGTGTACTCCTGT  2160
          ||||||||||||||||||||| |||||| ||||||||||||||||||| |||||||
Db  2222  TACGCCAGTGATCGTCTTGTTGCTGCTGTCAGTCAGCCAACCGTGACCCGTGTACTCCTGT  2281

Qy  2161  GGTTCTCTGTTCCCTAAGGCCCTGGATCTTCGGAGCCTTGTGTCCGCTCACGGGGCA  2220
          |||||||||||||||||| || ||||||| |||||| ||||| |||||||||| |||
Db  2282  GGCTCTCTCTTCCCCAAGGCCCTGGATCTTCGGAGCCTTGTGTCCGCTCAGGGGCA  2341

Qy  2221  CATAGCACCGGAGTCTTTTCCGTCCTGCTTGTTTTTACTTCGCCATTGCCAAC  2280
          |||||||||| |||||| |||||||||||||||| ||||| ||||||||||||
Db  2342  CACAGCACTGTGGTTGGTCTTTCAGTCTTGCTGTGTTGTCACCTCTGCCATCGCCAAC  2401

Qy  2281  ATGTTCACCTGTAACCACACCCCCATCACGGGAGTCGTGTCAGCCCGGATGCTGAATTTAACA  2340
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  2402  ATGTTCACCTGTAACCACACCCCCATCACCCGTGGGGAGTCGTGAGCCCGGATGCTGAATGTAACA  2461
```

Right column:

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Qy  2341  CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCTCGGATGCT  2400
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Qy  2401  CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATG  2460
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Qy  2461  CTGCTGAGTCCTTCTTGGCCAGCTGCTGCTTGTTTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
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Db  2582  CTGCTGAGTCCTTCTTGGCCAGCTGTCTGTTTTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2641

Qy  2521  ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTCTGCTGGGGTCCCCCAGCCACC  2580
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Qy  2581  ATCTTTGACAACTACTACTGCTTGGCCGTCCAGTGGCCTCTTCTTCCAATGAGACC  2640
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Qy  2701  ATTCTGCTGGTGTTGCGCTCCTGGCGCTGTATCTGCATGCTCAGCAGTGGAGTCGACTGCC  2760
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Qy  2881  CTGGCCCGGGAGCGCCCCAATGAGCAGATCTACTATCAGTCGTGTGGGTGGGCTGTT  2940
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Qy  3121  TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3180
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Db  3422  AAGCCACAGTATGACATCTGGGGGAACACGTGGAATGTCTCTTAGTCCGTATGGATGGACACG  3481

Qy  3361  GGGGTCCCCGACCAGTGGTCCAGGGGGTCAAGGTGAAGGGCAAGGGGAGGACCACCTAC  3420
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Qy  3421  TACCAGCTGGAGTGTCGAGGGTGTCAAGGTGAAGGGTCAAGGGTGAAGGTCAAGGGGAGGACCACCTAC  3480
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Db   3542 TACCAGCTGGAGTCGAGCGGTCGTGGTCAAGGTGAAGGCAAGGGGAGGATGACCACCTAC 3601
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RESULT 10
AX305965
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DEFINITION  Sequence 716 from Patent WO0188188.
ACCESSION   AX305965
VERSION     AX305965.1  GI:17645322
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
  TITLE     Method for examining ischemic conditions
  JOURNAL   Patent: WO 0188188-A 716 22-NOV-2001;
            School Juridical Person Nihon University (JP)
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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                     /db_xref="taxon:10090"
BASE COUNT     1214 a   1558 c   1673 g   1396 t
ORIGIN

Query Match       79.3%;  Score 2816.2;  DB 6;  Length 5841;
Best Local Similarity   87.8%;  Pred. No. 0;
Matches 3120;  Conservative   0; Mismatches   423; Indels   10; Gaps   4;

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Db     96 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTGTTCCCAAAGTGGATGAACGGAAAACAGCTTGGGGG 155

Qy     61 GAACGGCAATGGGCAGAGAGGTTCGCGGCGTGGCACTCGGGCGAGTGGCTTCTCGCACG 120
          |||||||||||||||||||||||||         ||||||||||||||||||  |||||||
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Qy    121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCGCAGAGCCCCAGCCCTGCGGGGCCCC 180
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Db    213 CCTGCTACATGAGCTGCCTCCTCAAGAATGCGAGACCCCCAGCCACCTGCCTGCGAGCTCAC 272

Qy    181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGCCGGCCAAGGGCAAGGCAAG 240
          |  |||||||||||||||||||||||||||||||||||||||| ||| ||  |||| ||||
Db    273 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCCGGAGGAGGGGCGGCCAGGGGTGTG 332

Qy    241 GAGCTGGGGCTGCGGGCAGTGGC 300
          |||||||||||||||||||||||
Db    333 GAGCTGGGGCTGCGGGCAGTGGCCTTGGGGTTTGACGACACTGAGGTGACCACCGATG 392

Qy    301 GGCGGGACCGGCTGAGGTGCGCGCCCGACGCGGTGGCCGCAT 360
          ||| | ||||||||||||||||||||||||||||  || |||
Db    393 GGC---ACAGCTGAAGTGGCACCGGATACATCGCC 449

Qy    361 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGTTCGAGCGGCCTGTAC 420
          |||||||||||||||||||||||||  || ||||||||||||||||||||  ||||||||
Db    450 CGGCTTGTCAGGTGTTCCAGTCTTAAGCAGTTCCCGGCCAAGTTGAGCGGCCTGTAC 509

Qy    421 CAGGCGGTACTTCTTCCAGATGAACCAGAGCAGCCAGCCTCGATGAGGGGGCTGCGTG 480
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Db    510 CAGGCGGTACTTCTTCCAGATGAACCAGAGCAGCCAGCCTCGATGAGGGGGCTGCGTG 569

Qy    481 CTGCTCAGCGCGGTGCGTCGTGGCTTCCACGCGCACCCGCCCCCCCAGCCTGCCTAT 540
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Db    570 CTGCTCATGGCTGTACTGTTGACTTTCCACGCTGCGCGCTGCCCAGCCTGCCTGCTTAC 629
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Qy    541 GTGGCACTGTTGGCCTGCCGCGCCCCTGTTGTGTGGGGCTCATGGTGGTGTGAACCGG 600
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Qy    601 CATAGCTTCCGCCCAGGACTCCATGTGGGTGGTGAGTTACGGTGCTGGCATCCTGGCG 660
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Qy    661 GCAGTGCAGTGCGGGCGCTCTGCCGCAGAGCACCGCGCAGCCCCCTCTGG 720
          |||| ||||| |||| ||||||||||||||| |||||||||||||||||||
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Qy    721 TGCCCTGTGTTCTTTGTCACATCGCCTACACGCTTCTCCCCATCCGGATCGGGGCTGCC 780
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Db    810 TGCCCGTGTTCTTCGTTCATCATCACTACACTCTTCTTCCCATTTCGCATCGCATGCGAGCCGCGCA 869

Qy    781 GTCCTCAGCGGCCTGGCCTTCCACCTTGCATTGATCTTGGCCTGGCAACTTAACCGT 840
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Db    870 GTACTCAGCGGCCTGGCCCTCGGGCCTCTCGGCCTTTGGCCTGGCAGCTCAACAGC 929

Qy    841 GGTGATGCTCCTCTGGAAGCAGCTCGGTGCCAATGTGCCGCTGCTGTTCCTCGCCACCAAC 900
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Qy    901 GTCATTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCAGCGCCTTTCAGGAG 960
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Qy    961 ACCCGCGGTTACATCCAGCCCGGCTCACCTGACCATGAGAATTCGGCAGCAGGAGCGG 1020
          ||||||||||||||||||| |||||||||||||||| || |||||||||||||||||||
Db   1050 ACCCGAGGTTACATCCAGCCCGGCGCGGCGCGGCTCAGCTGCACCTGCAGCAGGAGAGGACG 1109

Qy   1021 CTGCTGCTGTGGTATTGCCCCAGCAGTGTTGCCATGGCCAATGGATGAAAGAAGACATCAACACA 1080
          |||||||||||||||||||||||||||||||||||||| | |||| ||||||||||||||||||||
Db   1110 CTGCTGCTATCGGTGTTGCCCCAGCACGTTGCCATGGATGAATGAAAGAAGACATCAACACA 1169

Qy   1081 AAAAAAGAAGACATGATGTTCACAAGATCTACACAGATCATGTCAGCATC 1140
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Qy   1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGTGTCGCCGAGGCCCGG 1320
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Db  1767 GAGGAGAAAGCCATGCATGCTCGGCAACGGCTTCAGCGGACACGGACGCCAACTTCCATGGAAGGGACTG 1826

Qy  1741 ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGGCTTCCGC 1800
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Db  3027 ATGTTTGCCTCCATGCCAATTTCTCGGAGTTCTACGTGGAGCTCTCAGGCAAACAACACGAG 3086

Qy  3001 GGTGTCGAGTGCTGCCTGCGCGGCTCGCTGCTCAACGAGATCATCCTGACTTTGATGAGATTATCAGC 3060
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Db  3087 GGCGTGGAGTGCTGCCTGCTGGCTCGCTGCTCAATGAGATCATCCGACAGATACTTTCAACATCATCAGT 3146

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Db  3147 GAGGAGGAGATTCCGGCAGTTGGACAGTTGGAGAGATCAAGAACCATGGGTAGCACCACTAGTGGCGGCC 3206

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Qy  3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTAGTGATGACAGCACG 3360
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Qy  3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
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Db  3447 GGAGTTCCTGACCGAATCCAGGTGACTACGGACCTATACCAGGTTCTAGCTGCCAAGGGC 3506

Qy  3421 TACCAGCTGGAGTGTCGAGGGGTGTCAAGGTGAGCGGGGATGACCACCTAC 3480
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Db  3507 TACCAGCTGGAGTGTGTCGAGGGGTCGGGGTCAAGGTGAGGGAAAGGGGAGATGACCACCTAC 3566

Qy  3481 TTCCTCAATGGGGGGCCCCAGCCACC-AAATTCAGCTGAAGGGAC 3539
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Db  3567 TTCCTCAACGGGGGCCCCAGCAGTGCAGAGTGCAGCAGTTAGCACCGAGATTCAACCGAAGGAC 3626

Qy  3540 CAAGGTGGGCACT 3552
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Db  3627 CAAGGTGGGCATT 3639
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RESULT 11
MUSADCYC
LOCUS   MUSADCYC   5841 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION Mouse adenylyl cyclase type VI mRNA, complete cds.
ACCESSION   M93422
VERSION   M93422.1 GI:191690
KEYWORDS   adenylyl cyclase; adenylyl cyclase type VI.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE   1  (bases 1 to 5841)
  AUTHORS   Yoshimura,M. and Cooper,D.M.
  TITLE     Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
            from NCB-20 cells
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
  MEDLINE   92357702
   PUBMED   1379717
COMMENT     Original source text: Mus musculus cDNA to mRNA.
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                     AVQVGGALAANPHSPSAGLWCPVFFVYITYTLLPIRMRAAVLSGLGLSTLHLILAWQL
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                     AVGIFSVLLVFISAIANMFTCNHTPIRTCAARMLNLTPADVTACHLQQLNYSLGLDAP
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                     STARLDFLWKLQATGEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYYQSC
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                     GSTYMAASGLNASTYDQVGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLNMGP
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BASE COUNT     1214 a   1558 c   1673 g   1396 t
ORIGIN

  Query Match             79.3%;  Score 2816.2;  DB 10;  Length 5841;
  Best Local Similarity   87.8%;  Pred. No. 0;
  Matches 3120;  Conservative    0;  Mismatches  423;  Indels   10;  Gaps    4;

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Db       96 ATGTCATGGTTTAGTGGCCTCCTGGTTCCCAAAGTGGATGAACGGAAAACAGCTTGGGGG 155

Qy       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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Qy      121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
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Qy      181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
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Db      273 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCGGGCCCGGGCAGGGGTGTG 332

Qy      241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
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Db      333 GAGCTGGGGCTGCGGTCAGTGGCCTTGGGGTTTGACGACACTGAGGTGACCACACCGATG 392

Qy      301 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360
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Qy      361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 420
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Qy      421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGCGGTGCTGGTG 480
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Qy      481 CTGCTCACAGCGGTGCTGCTGGCTTTCCACGCCGCACCCGCCCGCCCTCAGCCTGCCTAT 540
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Qy      541 GTGGCACTGTTGGCCTGTGCCGCCGCCCTGTTCGTGGGGCTCATGGTGGTGTGTAACCGG 600
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Db      630 GTGGCCCTGCTGACCTGTGCCTCTGTCCTTTTTGTGGTACTCATGGTGGTGTGTAACCGA 689

Qy      601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTACGTGGTGCTGGGCATCCTGGCG 660
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Db      690 CACAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGCTATGTGGTCCTGGGCATCCTAGCA 749

Qy      661 GCAGTGCAGGTCGGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCCTCTGCGGGCCTCTGG 720
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Db      750 GCCGTGCAAGTCGGGGGTGCCCTGGCAGCCAATCCACACAGCCCCTCGGCGGGCCTTTGG 809

Qy      721 TGCCCTGTGTTCTTTGTCTACATCGCCTACACGCTCCTCCCCATCCGCATGCGGGCTGCC 780
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Qy      781 GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840
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Qy      841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAC 900
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Db      930 AGCGACCCCTTCCTTTGGAAGCAGCTCGGTGCTAACGTGGTGCTCTTCCTCTGCACCAAT 989

Qy      901 GTCATTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960
            | ||| ||  ||||||||||||| || || || |||||||||||||| || |||||||||
Db      990 GCCATCGGTGTCTGCACACACTACCCTGCTGAAGTGTCTCAGCGCCAAGCTTTTCAGGAG 1049

Qy      961 ACCCGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
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Db     1050 ACCCGAGGTTACATCCAGGCGCGGCTGCACCTGCAGCATGAGAACCGTCAGCAGGAACGG 1109

Qy     1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
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Db     1110 CTGCTGCTATCGGTGTTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1169

Qy     1081 AAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
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Db     1170 AAAAAAGAGGACATGATGTTCCATAAGATCTACATCCAGAAGCATGATAATGTCAGCATC 1229

Qy     1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTG 1200
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Qy     1201 GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1260
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Qy     1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
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Qy     1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1440
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Db 1530 CATTGCGGCGTCCTTGCCTACGGAAATGGCAGTTTGATGTCTGGTCAAGATGTGACC 1589

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Db 1590 CTGGCTAACCACCATGAGGAGGAGGCCGGGGGGC---GGCCGGCGCATCCACATCCGGCGGCTACA 1646

Qy 1561 CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCGCAACGCG 1620
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Qy 1741 ATGCCCGCCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTTCAAGGCCTTCCCG 1800
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Db 1827 ATGCCCCGCCTGGGTTCCTGACCGTGCCTTCCCGGACCAAGGACTCTAAGGCATTCCCGC 1886

Qy 1801 CAGATGGCATTGATGATTCAGCAAGACAACCGGGGCACCCGAGATGCCCTGAACCCT 1860
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Db 1887 CAGATGGGCATTGATGATTCTAGCAAAGAACAACCGGGGTGCCCAAGATGCTCTGAACCCT 1946

Qy 1861 GAGGATGAGGTGGATGAGTGTTCCTGAGCCGTGTCGCATCGATGATGTCTGATGATCAGCTG 1920
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Db 1947 GAAGATGAGGTGGATGAGTTCCTGCCGAGCCATCGAGTCCGAGCCATCGATACTCGGGATT 2006

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Qy 1981 TACTCCCGGAAGGTGATCGATCCCCGCTTCGGAGCCTACGTTGCCTGTCCCGTTGGTCTTC 2040
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Db 2067 TATTCACGGAAAGTAGATCCTCGCTTCGGAGCCTACGTCGCCTGTCCCGTCGTCCTGGTTTTT 2126

Qy 2041 TGCTTCATCGTCTTCCAGCTTCTCATCTTCCACCACCTCGATGCTTGGGATC 2100
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Qy 2281 ATGTTCACCTGTGAACCACACCCCCCATTAACGGCCGTGTGCAGCCCGGATGCTGAATTTAACA 2340
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Db 2487 CCCCTGTGTGAGGGAGCACCACCGCCACTCTTCCCTGAGTACTTCGTCGGGAACGTG 2546

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Qy 2641 TTTGATGGGCTGCAGACTGTCCAGCTGCTCCAGCGGAGGGGTGGCCCTCAAATATGACCCCTGTG 2700
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Db 2727 TTTGATGGGCTGGACTGGCCCAGCTGTCCAGCTTCTCAAATATATGACCCCCACCTG 2786

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Qy 2821 CAGGCATACAACCGAGGAGCGCTGCTGCATAACATTCTGCCCAAGGACTTGGCCGCCCACTTC 2880
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Db 2907 CAGGCATACAACCGAGGAGGTTGCTGCATAACATTCTTCCCAAGGACGCGGGCCGCCCACTTC 2966

Qy 2881 CTGGCCCGGAGCGCGCCGCAATGAATGATGAACTCTACATCAGTCGTGTGTGAGGCTGCC 2940
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Qy 3001 GGTGTCGAGTGCTCCGGCGGTTCGGGCAGCTTCGACATCGCTGACTTTGACGATTATCAGC 3060
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Db 3087 GGCGTGGAGTGCTCCGGCTGGTTCATGGAGCTCTGACGACTTTGACGAGATCATCAGT 3146

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Qy 3121 TCAGGGCTGAACGCCAGCACCTACGATCAGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
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Db 3207 TCTGGGCTAAATGCCAGTGCCACCTATGACCAGTGGCGGCGCGTCCCGCTCACACACGGCGGCTGGCT 3266

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Qy 3540 CAAGGTGGGCACT 3552
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Db 3627 CAAGGTGGGCATT 3639

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DEFINITION   Sequence 11 from patent US 6107076.
ACCESSION    AR106659
VERSION      AR106659.1  GI:12821189
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 4131)
  AUTHORS    Tang,W.-J. and Gilman,A.G.
  TITLE      Soluble mammalian adenylyl cyclase and uses therefor
  JOURNAL    Patent: US 6107076-A 11 22-AUG-2000;
FEATURES             Location/Qualifiers
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BASE COUNT      835 a   1190 c   1182 g    924 t
ORIGIN

Query Match           79.1%;  Score 2810.4;  DB 6;  Length 4131;
Best Local Similarity 87.5%;  Pred. No. 0;
Matches 3110;  Conservative 0;  Mismatches 436;  Indels 8;  Gaps 3;
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Qy   61 GAACGCAATGGGCAGAAGCGTTCGCGGCGGCTTCGGGCAGTGGCTTCTGCACG        120
        ||||||||||| ||||||||                          |||||||||| |||
Db  116 GAACGCAATGGACAGAAGCGG---CCCACGCGCAGGCGACCCGAGCCCGTGGCTTCTGCGCG 172

Qy  121 CCCCGCTATATGAGCTCCGGGATGCAGAGCCACCCAGCCCCTGCGGGCCCC          180
        |||||||| | |||||||  |                    |||||||||||
Db  173 CCCCGCTACTACATGAGCTGCTCCCGGGGGTGCCGGAGCCCCAGCCCCACTCCTGCAGCTGC 232

Qy  181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAG       240
        | |||||||||||||||||||||| ||||||||| ||||||||| |||| |||
Db  233 ACTCGGTGCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGGCTGCCCGGGGGTGTG      292

Qy  241 GAGCTGGGGGCTGCGGGCAGTGCGCCCTGGGCCTCTGAGGATACCGAGGTGACAACAGACGCG 300
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Db  293 GAGCTGGGGCTGCGCGGTCAGTGCGCCGGTGTTTGATGACACTGAGGTG---ACCACACCG  349

Qy  301 GGGCGGCGACGGCTGAGGTGGCGCCCGACGCGGGTGGCCGAGAGTGGCGATCCTGCTGCGCG 360
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Db  350 ATGGGACAGCTGAGGTGGCACCCGACACATCGCCGTCCGGTCCGCTGCTGGCAC        409

Qy  361 CGTCGGTGCTGCAGGTGTTCCAGTGCGAAGCAGTTCCGTTCCGGTTCGGCAAGCTGGAGCGCGGCCTGTAC 420
        ||||||||| |||| |||||||||| |||||||||| |||| | ||| ||||||||||||||| ||||||||
Db  410 CGGTCAGCGCAGGTGTTCCAGTCCGATGGAGGTGGTCTTAAGCAGTTCCCGTTCCCGGTCGTGTACTAC    469

Qy  421 CAGGGGTACTTCTTCCAGATGAACCAGAGCAGCGAGGGGTTCAGCCTGTGATGGCGGTGCTGGTG 480
        |||||||||||||||||| ||||||| |||  |  | |||| |  |  | ||| | |||
Db  470 CAGGGGTACTTCTTCCAGATGAACCAGAGCAGCGAGGGGCTATGTGTTCGGGGCATCCTCAGCA 529

Qy  481 CTGCTCACGCGGTGCTGGCTGCTTTCCAGCCGGTGCTGGCCCCCGCCCCCGC       540
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Db  530 CTCTCCATGGCTGTACTGTGACCTTTGACGTTGCACTGTGAGCCTGTGGGCTAT       589

Qy  541 GTGGCACTGTTGGCCCTGTGCGCCGCCCCTGTTCCGTTCGTGGGGCTCATGTGTGTGTGTAACCGG 600
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Db  590 GTGGCACTGCCGGACCCTGACCGTCCTGTCCTTTTTTTGTGGTACTCATGGTAGTGTGTAACCGA 649

Qy  601 CATAGCTTCCGCCCAGGACTTCCATGTGGGTGTAGTTACGTGGTGTGGCCACATCCTCGGCG 660
        |||||||||  |||||| |||||| | | | |  | |  | | | || | |||||| |||||
Db  650 CATAGCTTCCGCCCAGGACTTCCATGTGGGTGTAGTGAGCTATGTGGGTTCGGGCATCCTAGCA 709

Qy  661 GCAGTGCAGGTCGGGGGGCGGCGGCCCTCTGCAGCAGCACCCCGCAGCCCCTGCGGGCCCC 720
        ||||||||||||||||||||| | | |  |  |  ||||| |    |||||||||||||
Db  710 GCCGTGCAAGTCCGGGGGGTTGCCCTTGGCACTGCACCCAACCCAGCCCAGCAGCCCTTTGG 769

Qy  721 TGCCCGTGTTCTTTGTCTACATCGCCTACACGCCTCTCCCCATCCGCATCGCCTCGCTGCC 780
        ||||| |||| | |||| ||| ||| || |  |||| | | ||||| | | |  |  | ||
Db  770 TGCCCCGGTTCTTTGTCGTCTTACCTCACACTTCTTCCCATTCCCATTCGTATGCCGAGCCC 829

Qy  781 GTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTGATCTTGGCCTGGCAACTTAACCGT    840
        || ||||| |||||||||||||  ||||  ||||||| |||| | |||||||||| |||
Db  830 GTGCTCAGTGGCCTGGGCCTCTTTCCACCCTGCATTGATTTTGATTTTGGCCTGGCATCTCAACAAT 889

Qy  841 GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCCTCGCACCAAC   900
        |||||   ||||||| ||||||||||||||||| || ||| |  |||||| |||||||
Db  890 GGTGACCCCTTCCTTTGGAAGCAGCTCGGTGCTAACGTGGTCGTCTTCCTGTGCACCAAT 949

Qy  901 GTCATTGGCATCTGCACACATCATCGACAGAGAGGTGTCTCAGCAGGTTTCAGGAG    960
        | |||||| ||||||||  ||  |   | ||| ||||||||||| | | |||||||||
Db  950 GCCATCGGTGTCTGCACGCACTACCCCGTGAAGTGTCTCAGCGCGCCAAGCCTTTCAGGAG 1009

Qy  961 ACCGGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGGCGG 1020
        ||||| ||||||||||||||||||||  |||||||||||||||||||| |||||||| |||
Db 1010 ACCGGTGGTTACATCCAGGCCCGGCTGCACTTGCAGCATGAGAATCGACAGCAGGAACGG  1069

Qy 1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAGAAGACATCAACACA  1080
        |||||||||||||| |||||||||||| |||||||||| |||||| ||| ||| ||||||
Db 1070 CTGCTGCTGTCGGTGTTGCCCCAGCATGTTGCCATGGAAATGAAAGAGGATATCAACACA 1129

Qy 1081 AAAAAGAGAACATGATGTTCCACAGATCTACATACAGAGCAATGACAATGTCAGCATC   1140
        |||||| | |||||||||||||||| || |||||||| |||| | |||||| ||||||||
Db 1130 AAAAAGGAAGACATGATGTTCCACAAGATTTACATCCAGAAGAAGCATGACAATGTCAGCATC 1189

Qy 1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCTGCATCCCCAGTCGACTGCGCCAGGAGCTG  1200
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Db 1190 CTGTTTGCCGACATCGAGGGCTTCACCAGCTGCATCCCCAGTCGACTGCGCCCAGGAACTG 1249

Qy 1201 GTCATGACCCTGAATGAGTCTTTGCCCGGTTTGACAAGCTGGCTGTGCGCGGAGAATCACTGC 1260
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Db 1250 GTCATGACCTTGAATGAGTCTTTGCCCGGTTCGACAAGCTGGCTGTGCGCGGAGAATCACTGT 1309

Qy 1261 CTGAGGATCAAGATCTTGGGGACGTGTTACTACTGTGTGTGTCAGGTTGCGGGGCCCGG   1320
        ||||||||||||||||| || ||| |||||||||||||||||  | | || ||| ||||||
Db 1310 CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGTGTGTGGCGGCTGCTGCGGAGGCCCGG 1369

Qy 1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG  1380
        || ||||||||||||  ||||||||||||||||||||||||||| ||||||||||||||||
Db 1370 GCAGACCATGCCCACCTGCTGTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG 1429

Qy 1381 GTACGTGAGGTGACAGGTGAATGTGAACATGCGGCGCATCCACAGCGGGCGCGTG      1440
        || ||||||||  | |||| | ||||||||||||||||||||||||||||||| ||
Db 1430 GTGCGTGAGGTAACGGGTGTAAATGTGAACATGCGGCGCATCCACAGCGGGCGCGGTA   1489

Qy 1441 CACTGTGGCGGCGTCCTTGGCTTCGGCTTCCGTTCCGCAAGCTGGAGCGCTGTGACC   1500
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Db 1490 CACTGCGGTGTCCTTGGTCCTTCGTCCGCAAGCTGGAGCGCTGTGACC           1549

Qy 1501 CTGGCCAACCACCATGGAGGCAGGAGGCCCGGCCTGCGAGCTGCTGATGGCGGTGCTGGTG 1560
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Db 1550 CTGGCCAACCACCATGGAGGCGGCGGCGGCCCGGCCTGCGAGCTGCTGATGGCGGTGCTTGTG 1609

Qy 1561 CTGAGTACCTGACACGGGACTACGAGGTGGAGCCGGCAGCCGGCCCTGCTGCTAT       1620
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Db 1610 CTGCAGTACCTGACTGGGGACTATGAGGTGGAGCGGGCGGTGAGCGCAACGCG      1669

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Db 1730 GAGGAGAAGGCCATGCTGGCCAAGCTCAAGCTGCGCAAGCTGCGCCAACTCACTCGGGAAGGGACTG 1789

Qy 1741 ATGCCGCGCTGGGTTCCTGATCGTCGTGCCTTCTCCCCGGACACTCAAGGACTCCAAGGCCTTCCGC 1800
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Qy 1801 CAGATGGCATTGATGATTCCAGCAAAGACAACGGGGCACCCGGACACCGCATGCCTGAACCCT 1860
        |||| || |||||| ||| | |||||| ||| ||| |  ||| || |||| | || |||||||
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Qy 1861 GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGAGCCCGAGCCATTGATCAGCTG 1920
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Qy   1910  ||||||||||||| |||||| ||||| ||| |||| |||||  |||| |||||||||||||  1969
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Qy   1921  CGGAAGGACCATGTGGCGCCGGTTTCGTCGCTTGCGTTGTGCTGCTGCTTGAGAAGAAG  1980
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           CGTAAGGACCATGTGGCGCCGGTTCCGTCGCTTCCGCTGCTTCCGAGAGGGAGGAGAAG  2029

Qy   1970                                                                2029
Db

Qy   1981  TACTCCCGGAAGGTGATCCCGCGTTCGGAGCCTACGTTGCTGTGCCCTGTTGGTCTTC  2040
Db         |||||| ||||| ||||| |||||| ||||| ||||| ||||| |||||||||||||
           TATTCACGGAAAGTAGACCCTCGTTTCGGAGCCTACGTCGCGCTGTGCCCTGTGTTTTC  2089

Qy   2041  TGCTTCATCTGCTTCATCCAGCTTCCACACTTCCACCTTCCACCCTGATGCTTGGGATC  2100
Db         |||||||||||| ||||| |||||||||||||||||||||| |||||||||||||||
           TGCTTCATCTGTTTCATCCAGCTTCCACACTTCCGCCCCGATACTCGGGATT  2149

Qy   2101  TATGCCAGCATCTTCCTGCTCGTGCTAATCACCGTCGATCTGTGTGTACTCCTGT  2160
Db         ||||| | |||||| ||||| |||||| |||||||||||||||||||||||||||
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Qy   2161  GGTTCTGTTCCCTAAGGCCCTGCGAACGTCGTCCCGCAGCATTGTCCCGCTCACGGGCA  2220
Db         ||||||||||||||||||||| ||||| |||||||||||| |||||||||||||||||||
           GGGTCTTTCTTCCCCAAGCCCTGCGAGCGCGCCCGCAGCCGCAGTATCGCCCGCTCACGGGGTG  2269

Qy   2221  CATAGCACCGCAGTTGGCATCTTTCCGTCCTGCTGTGTTTACTTCTGCTCATTGCCCAAC  2280
Db         | |||||||||||||||| ||||||| |||| |||||||  ||| ||||| ||||||||||
           CACAGCACCGCGTGTTGGAGTCTTCTCGGGTTCTCGGTTGTTCATCTCTGCCATTGCCCAAC  2329

Qy   2281  ATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTAACA  2340
Db         ||||| ||| |||||| ||| ||| |||||||||| |||| ||||||||||||||||||
           ATGTTCACCTGACCAGTACACCCCCACTGAGGACCTGAGACGATCTCTACCAGGTTCTACCAGGGGC  2389

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           CCGTCCGATGTCACCGCCTGCCACTACGACCTCAATTACTCTCTGGGGACTGGAAGCT  2449

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Qy   2521  ATGATCTTTGTCTTGGGCTCATCTATTCGTGCTGCTTCTGCTGCTGGTCCCCAGCCACC  2580
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Qy   2581  ATCTTTGACAAACTATGACCTACTGCTTGGCGTGCCATGAGCCTTCTTCCAATGAGACC  2640
Db         ||||||||||||||||||| |||||| ||||||||| |||||| |||||||||||||||
           ATCTTTGACAACTATGATCTACTGCTTAGCGGTCCATGGCCTTTGGCTTCCTCCAATGAGACC  2689

Qy   2641  TTTGATGGGCTGACTGTCCAGCTGCAGGGAGGGGTGGCCCTCAAATATATGACCCCTGTG  2700
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           TTCGATGGGCTGGACTGGCCAGCCGGTAGGGGTAGCGCCTCAAATACATGACCCCGTG  2749

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Db         |||||||| |||||| ||||| ||||| ||||| ||| |||||||| ||||| |||||||||
           ATTCTCCTCGTTCGTGTTCCGCCCTGCCACTGTATCGTACTCACACGGGGAATCTACCGCGCC  2809

Qy   2761  CGCCTAGACTTCCTCTGGAAACTACAGGCCAACAGAGGGGAGAGGAGGAGAGCTA  2820
Db         ||||| |||||||||| ||||||||||| ||||| |||||||||||||||||||
           CGCCTGGACTTCCTGTGGAAACTGCAGGGGAGGGGAGAAGAGGAGAGAGTTG  2869

Qy   2821  CAGGCATACAACCGGAGGCTGCTGCATAAATTCTGCCCAAGGACCTGGCGGCCACTTC  2880
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           CAGGCCTACAACCGGGGCTGCCTGCTGCATAAATGAGGACCTGCCCCACTTC  2929

Qy   2881  CTGGCCCGGAGCGCCGCCAATGATGAACTCTACTATCAGTGCGTGTGAGTGTGCTGTT  2940
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           CTGGCCCGGGAGGCGCCGCCAACGACGTGCTGCTACCCAATCCTGCCGAGTGCGTGGCGTC  2989

Qy   2941  ATGTTTGCCTCCAACTTCCTCTCGAGTTCTATGTGGAAGCTGGAGCAAACAATGAG  3000
Db         ||||||||||||||||||||| |||||| ||||||||||||| ||||||||||||||
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Db   2990  ATGTTTGCCTCCATCGCCAACTTCTCTGAGTTCTATGTGGAACTGGAGGGCGAACAATGAG  3049

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Qy   3121  TCAGGGCTGAACGCCAGCACCTACGATCCAGTCAGGTGGGCGCTCCCCACATCACTGCCCTGGCT  3180
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Qy   3241  TTCCAGATGAAGATTGGGCTGAACATGGGCCACTCGTGGCAGTGTGTCATCGGGCTCGG  3300
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Qy   3301  AAGGCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTTAGTGTATGGACAGCACG  3360
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Qy   3421  TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAACGGGGAGATGACCACCTAC  3480
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           TACCAACTGGAGTGTCGAGGGGTGGTCAAGGTGAACGGGGAGAGATGACCACCTAC  3529

Qy   3481  TTCCTCAATGGGGCGCCCAGCAGTTAACAGGGCCCA--GCCACAAATTCAGCTGAGGGA  3538
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           TTCCTCAATGGGGCCCCCCAGCAGTTAGCAGACGCGCACGAGTGGAAATTCAACCAAAGGGA  3589

Qy   3539  CCAAGGTGGGCACT  3552
Db         ||||||||||||||
           CCAAGGTGGGCACT  3603
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RESULT 13

RATADCYB
LOCUS   RATADCYB   4131 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
ACCESSION   M96160
VERSION   M96160.1 GI:202718
KEYWORDS   adenylate cyclase; adenylyl cyclase type VI.
SOURCE   Rattus norvegicus (Norway rat)
  ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 4131)
  AUTHORS   Premont,R.T.
  TITLE   Multiple mechanisms underlying desensitization of the liver
            adenylyl cyclase system. Structure and cAMP regulation of liver
            adenylyl cyclases
  JOURNAL   Thesis (1992)
REFERENCE   2 (bases 1 to 4131)
  AUTHORS   Premont,R.T., Chen,J., Ma,H.W., Ponnapalli,M. and Iyengar,R.
  TITLE   Two members of a widely expressed subfamily of hormone-stimulated
            adenylyl cyclases
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
   MEDLINE 93028552
   PUBMED   1409703
COMMENT   Original source text: Rattus norvegicus (strain Sprague-Dawley)
            adult liver, kidney, heart cDNA to mRNA.
FEATURES   Location/Qualifiers
     source   1..4131
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            VLAAKGYQLECRGVVKVKGKGEMTTYFLNGGPSS"
BASE COUNT       835 a     1190 c     1182 g      924 t
ORIGIN

Query Match       79.1%;   Score 2810.4;  DB 10;   Length 4131;
Best Local Similarity   87.5%;   Pred. No. 0;
Matches 3110;   Conservative   0;   Mismatches  436;   Indels   8;   Gaps   3;
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Qy   1561  CTGCAGTACCTGAACCGGGACTACGAGGTGGAGCGCCAGGCCGTGGTGGGAGCGCAACGCG  1620
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Db   1610  CTGCAGTACCTGAACCGGGACTATGAGGTGGAGCGCCAGGCCGTGGTGGGAGCGCAACGCG  1669

Qy   1621  TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCGCCAGCCCAGAAACGGAAA  1680
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Qy   1681  GAGGAGAAGGCCATGTCGGCCAAGCTGCGGCGACTCGGGCGACTTCCATGGAAGGCTG  1740
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Db   1730  GAGGAGAAGGCCATGTCGGCCAAGCTGCAGCGGACGCGGCCAACTCCATGGAAGGACTG  1789

Qy   1741  ATGCCCGCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTTCCAAGGCCTTCCGC  1800
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Db   1790  ATGCCCGCTGGGTTCCTGACCGTGCCTTCCCCGGGACCAAGGACTTGCCATGGCATTCCGA  1849

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Db   1850  CAGATGGGCATCGATGACTCTAGCAAAGAGAACCGGGGTGCCCAAGATGCTCTGAAACCCT  1909

Qy   1861  GAGGATGAGGTGGATGAGTTCCTGAGCCGTTCCGACGTCCCATCGATGATCGATCAGCTG  1920
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Qy   1921  CGGAAGGACCATGTGCCCGGTTTCTGCTCACCTTCCACACCTTCCCACCTCCAGAGAAGAAG  1980
           ||||||||||||||||||| |||| |||||| |||||| |||||| |||||||||||||||
Db   1970  CGTAAGGACCATGTGCCCGGTTCCGGCCGTTCCCGAGCGCTAGTCGCCACCTTCCGAGAAGAAG  2029

Qy   1981  TACTCCCGGAGGTGATCCATCCTGCTTCGGAGCCTTACGTTGCCCTGTTGGTCTTC  2040
           |||||| ||||| ||||||||||| || |||||||||| ||||| |||| ||||||
Db   2030  TATTCACGGAAAGTAGACCCTCGTTTCGGAGCCTAGTCGCGCCTGTCGCCCTGTTTTC  2089

Qy   2041  TGCTTCATCTGCTTCATCCAGCTTCTCCACAGTTCCCACCTCCACCCTGGGATCGCTTGGGATC  2100
           |||||||||||||||||||||||| | |||||| |||||||||||||| | |||||| |||| |
Db   2090  TGCTTCATCTGTTTCATCCAGTTCCTCCACACTTCCGCGCCCTGATACTCGGGATT  2149

Qy   2101  TATGCCAGCATCTTCCTGCGTGCTAATCACCGTGCTGATCTGTGCTGTCTCCTGT  2160
           |||||||||||||||||||||| ||||| ||| || |||||| ||||||||||||
Db   2150  TATGCCGGGATCTTCCTTGTCGCGTGGTCACCGTGCTCATCTCGTGTGCTGTCTCCTGT  2209

Qy   2161  GGTTCTGTTCCCTAAGGCCCTGCGAACGTCTGTCCCGCTCACGGGCA  2220
           |||| |||||||||| |||| ||||||| ||| ||||| || |||||
Db   2210  GGGTCTTTCTTCCCCAACGCCCTGCGAGCGCCTGTCGCCGTATCGCGCTCACGGGGTG  2269

Qy   2221  CATAGCACCCGAGTTGGCATCTTTCCGTCGTGTTTACTTCTGCCATTGCCAAC  2280
           |||||||| |||||||||||||||||||||| |||| || |||||||||||||
Db   2270  CACAGCACACGCGGCTGTTGGAGTCTTCGTCGTGTTTGTTCATCTCTGCCATTGCCAAC  2329

Qy   2281  ATGTTCACCTGTAACCACACCCCCATACGGAGCGTGCAGCCCGGATGCTGAATTTAACA  2340
           ||||||||||| || |||| |||||||||||| ||||||||| || || ||||||||||
Db   2330  ATGTTCACCTGACCGAGTCACACCGCCACACCGGAGCGTGCAGCCCGATGCTGAACTTAACA  2389

Qy   2341  CCTGTGACATCACTGCCTGCCAGCTCAATTACTCTCTCGGGCCTGATGCT  2400
           |||||||||||| ||||||||||||||||||||| || ||||||||||||
Db   2390  CCGTCGACATGTCACCGCCTGCCAGCTCAATTACTACTCTCTCGGGACTGGAAGCT  2449

Qy   2401  CCCCTGTGTGAGGCGCCCCAGCACCATGCCCACCCCACCCACCATGGGGAACATG  2460
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Db   2460  CCCCTGTGTGAGGGCCCCCAGCCCCCGCACCGCCACCGACCATTTGTCGGGGAGTGTG  2509

Qy   2461  CTGCTGAGTCTTTGGGGCTCATCTCATTATTTGGTGCTGCTTCCTGCTGGGTCTCCCCCAGCCACC  2520
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Db   2510  CTGCTGAGTCTTTGGGGCTCTTGGCCAGCTCCGGCCACCCGTCCTTCCGTCCTCGGGTTCCCCCAGCCACC  2569

Qy   2521  ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCCTGCTGGGTCCCCAGCCACC  2580
           ||||| |||||||| ||||| ||||| |||||||||||||||| ||||||||||||||||
Db   2570  ATGAACTTTGTCTTGGGGTTCATCTACTTTGTCTGGTTTGCTGCTTCCTGCTGGGTCCCCAGCCACC  2629

Qy   2581  ATCTTTGACAACTATCATGACCTACTGCTTGGCCGTCCATGGCTTGGCTTCTTCAATGAGACC  2640
           ||||||||||||||||| |||||||||||||| ||||| |||||||||||||||||||||||
Db   2630  ATCTTTGACAACTATGATCTACTGCTTAGCCGTCCATGGCTTGGCTTCTTCCCTCCAATGAGACC  2689

Qy   2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGGTGGCCCTCAAATATGACCCCGTGTG  2700
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Db   2690  TTCGATGGGCTGGACTGCCCAGCCTGACCGGTAGGGGAGGGGTAGCGCTCAAATACATGACCCCTGTG  2749
           |||||||||||||||| |||||||| || || |||||||||||| |||||||| ||||| ||||||||

Qy   2701  ATTCTGCTGGTGTTGCGCTGGCGCCTGTATCTGCATGCTCAGCAGCTGGAGTCGACTGCC  2760
           |||||||||| ||| || || |||||| |||||||||| ||||||| || |||| |||||
Db   2750  ATTCTCCTCGTGTTGCCCTGGCTGGACTGTATCTACACGGACACCAGGTGGAATCTACCGCC  2809

Qy   2761  CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGGAAGAGGAGGAGGAGCTA  2820
           | ||| |||||| || |||||||||| || |||||| |||||||||||||||||||
Db   2810  CGCCTGGACTTCCTGTGAAACTGCAGGCCACAGGGAGGAAGAGGAGGAGGAGGAGTTG  2869

Qy   2821  CAGGCATCACAACCAGGAGGCTGTCGCATACAATCCTCCCAAGACGTGCGGCCCACTTC  2880
           ||||| | |||||||||||||||||| | ||||||| || ||||||||||||||||||
Db   2870  CAGGCCTACAACCGGGACGGCTGTGCATAACATCCTTCCCAAGACGTGCTGCCCACTTC  2929

Qy   2881  CTGGCCCCGGAGCCCGCCAATGATGAACTTCACTATCAGTCGTGTGAGTGTGGCTGTT  2940
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Db   2930  CTGGCCCCGGAGCCCGCCAACGACGAGTGTACTACCAATCCTCGCGAGTGGCTGGCTGTC  2989

Qy   2941  ATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  3000
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Db   2990  ATGTTTGCCTCCATCGGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCCGAACAATGAG  3049

Qy   3001  GGTGTCGAGTGCCGCTGCCAGCTGGAAAAGATCAACGAGTCATCGACTCTTGATGAGATTATCAGC  3060
           || ||||||||||| |||||||||| |||||| ||||| ||| || |||||| ||||| |||||||
Db   3050  GGCGTGAGTGCCGCTGCCAGCTGGAGAGATCAAGATGCTGACTTTGACTCATCATCAGT  3109

Qy   3061  GAGGAGCCGTTCCGGCAGCTGGAGAAAGATCAAGACAGTGGGCCGTCCCCACATCACTGCGCCTGGCT  3120
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Qy   3121  TCAGGGCTGAAGCCAGCCACTACGATCAGGTGGGCGGTCCCCACATCTGCCCCTGGCT  3180
           |||| || ||| ||| ||||||||||||| ||||| || ||||||||||||||||| |
Db   3170  TCCGGGCTAAATCCAGCACCTATGACCACCATGCTCCGGCCCGCTGCCATCAACAAT  3229

Qy   3181  GACTACGCCATGCGGCTCATCATGAGCAGCAGAATCAATGACCACACTTCCTTCAACAAT  3240
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Db   3230  GACTACGCCATGCGGCTTATGAGCAGCAAATGAAACACATCTTTCAACACC  3289

Qy   3241  TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTGTGCAGTGTCATCGGGGCTCGG  3300
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Db   3290  TTCCAGATGAAGATCGGGCTTGAACATGGGTCCGGTTGCAGTGTCATTGGGGCCCCGG  3349

Qy   3301  AAGCCACCAGTATGACATCTGGGGGAACACAGTGAAATGTCTCTAGTCGTATGGACACACG  3360
           ||||| || |||||| |||| ||||||| | |||||| || ||| ||||| ||||| |||
Db   3350  AAGCCACCAGTATGACATCTGGGGGAAACACGGTGAAATGTTGAATGTTCCAGCCGTATGGACAGCACA  3409

Qy   3361  GGGGTCCCCGACCGAATCCAGGTGACCAGCGACCTGTACCAGGTTCTGCCAAGGGC  3420
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Db   3410  GGAGTTCCTGACCGAATACAGGTGACCACCGATCTCTACCAGGTTCTGCCAAGGGC  3469

Qy   3421  TACCAGCTGGAGTGTCGAGGGTCGTCAAGGTGCAAGGGGGAGAGTGACCACCTAC  3480
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Db   3470  TACCAACTGGAGTGTCGAGGGGTCGTCAAGGTGCAAGGGGAAAGGGGGAGGATGACCACCTAC  3529

Qy   3481  TTTCTCAATGGGGCGCCCCAGCCCCCA--GCCCAAATTCAGTCGTGAAGGGA  3538
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Db   3530  TTTCTCAATGGGGCGCCCCAGCCCCCAGCACGAGCGCACCGAGTGGAAATTCAACCAAAGGGA  3589

Qy   3539  CCAAGGTGGGCACT  3552
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Db   3590  CCAAGGTGGGCACT  3603
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RESULT 14

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RATADC
LOCUS       RATADC                    6036 bp    mRNA    linear    ROD 12-AUG-1994
DEFINITION  Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
ACCESSION   L01115
VERSION     L01115.1  GI:202712
KEYWORDS    adenylate cyclase; adenylyl cyclase; adenylyl cyclase type VI.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 6036)
AUTHORS     Krupinski,J., Lehman,T.C., Frankenfield,C.D., Zwaagstra,J.C. and
            Watson,P.A.
TITLE       Molecular diversity in the adenylylcyclase family. Evidence for
            eight forms of the enzyme and cloning of type VI
JOURNAL     J. Biol. Chem. 267 (34), 24858-24862 (1992)
MEDLINE     93077589
PUBMED      1332969
COMMENT     Original source text: Rattus norvegicus hepatoma cDNA to mRNA.
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                     MAVLLTFHAAPALPQPAYVALLTCASVLPVVLMVVCNRHSFRQDSMWVVSVVVLGILA
                     AVQVGGALAANPRSPSAGLWCPVFVYIYTTLLPIRMRAAVLSGLGLSTLHLILAWHL
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     polyA_site      6036
BASE COUNT     1223 a   1657 c   1750 g   1406 t
ORIGIN

Query Match              78.9%;  Score 2802.4;  DB 10;  Length 6036;
Best Local Similarity    87.4%;  Pred. No. 0;
Matches  3105;  Conservative    0;  Mismatches  441;  Indels    8;  Gaps    3;

Qy    1  ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT  60
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Db  199  ATGTCATGGTTTAGGGGCCTCCTGGTTCCCAAAGTGGATGAACGGAAAACAGCCTGGGGC  258

Qy   61  GAACGCAATGGGCAGGAGAGCGTTCGCGGCAGAGAGC---CCCACGCCAGGCGACCCGGC  120
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Db  259  GAACGCAATGGGCAGGACAGAGCG------CCCACGCCAGGCGACCCGGCCTTCTGCGCG  315

Qy  121  CCCCGCTATATGAGCTGCCTCCCGGGATGCAGAGCCACCACCCCAGCCCCGGGGCCCC  180
         ||||||||| ||||||||||| || |||| |||||||||||| ||||| ||| || |||
Db  316  CCCCGCTACATGAGCTGCCTGCCTCAAGAATGTGGAGCCACCACCTCCTGCGCC  375

Qy  181  CCTCGGTGCCCCCTGGCAGGATGACGCGCCTTCATCCGGGGGCTGCGGAGGGGCAAG  240
         | ||||||||||||||||||||||| || ||||||| ||| |||||||||||||| ||
Db  376  ACTCGGTGCCCCCTGGCAGGATGAAGCCTTCATCAGGAGGGCTGCGGAGGGGCGTG  435

Qy  241  GAGCTGGGGCTGCGGGAGCAGTGGGCCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG  300
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[The following rows continue the Qy/Db nucleotide alignment; positions shown at left (start) and right (end) of each sequence line, with the match bars (|) between paired Db and Qy lines.]

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Db  436 ... 492
Qy  301 ... 360
Db  493 ... 552
Qy  361 ... 420
Db  553 ... 612
Qy  421 ... 480
Db  613 ... 672
Qy  481 ... 540
Db  673 ... 732
Qy  541 ... 600
Db  733 ... 792
Qy  601 ... 660
Db  793 ... 852
Qy  661 ... 720
Db  853 ... 912
Qy  721 ... 780
Db  913 ... 972
Qy  781 ... 840
Db  973 ...1032
Qy  841 ... 900
Db 1033 ...1092
Qy  901 ... 960
Db 1093 ...1152
Qy  961 ...1020
Db 1153 ...1212
Qy 1021 ...1080
Db 1213 ...1272
Qy 1081 ...1140
Db 1273 ...1332
Qy 1141 ...1200
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Qy 1201 ...1260
Db 1393 ...1452
Qy 1261 ...1320
Db 1453 ...1512
Qy 1321 ...1380
Db 1513 ...1572
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Qy 2461 CTGCTGAGTCTTCTTGGCCAGCTCTGTCTTCCTGCCACATCAGCAGCATCGGCAGCGAGTTGGCC 2520
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Db 2653 CTGTTGAGTCTTCTTGGCCAGCTCCGTCTCCTGCTTCCTCGTTCTCTGGTGCTCGCTGGCTAGTT 2712

Qy 2521 ATGATCTTTGTCTTGGGCTCATCTATTTGTCGTTGTGCTCGTCTGCGTCCCCAGCCACC 2580
         |||||||| |||| ||||||||||||||||||| || |||||||||||||||||||||||
Db 2713 ATGACCTTTGTCTTGACGTTCATCTACTTGTCGTTTGCTCGTCTGCGTCCCCAGCCACC 2772

Qy 2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
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Db 2773 ATCTTTGACAACTATGATCTACTACTGCTTAGCGTCCATGGCTTGGCTTCCTCCAATGAGACC 2832

Qy 2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGTGGCCCTCAAATATGACCCCTGTG 2700
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Db 2833 TTCGATGGGCTGGACTGCCCAGCCGTAGGGAGGTAGCGCCTCAAATACAGTACCCCCTGTG 2892

Qy 2701 ATTCTGCTCGGTGTTTGCCGCTGGCGCGTGTATCTGCATCTCAGCAGGTGGAGTCGACTGCC 2760
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Db 2893 ATTCTCCTCGTGTTCGCCCTGGCACTGTATCTGTATCTCACACGGCACACAGGGTGGAATCTACCCGCC 2952

Qy 2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGGAGGAGGAGGAGGAGGAGCTA 2820
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Db 2953 CGCCTGGACTTCCTCTGTGGAAACTGCAGGCCACAGAGGGAGGAGGAGGAGGAGGAGGAGTTG 3012

Qy 2821 CAGGCATACAACCGGAGGCTGCTGCAATGACTCTTCTCGCCCAAGGACGTGGCGGCCACTTC 2880
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Db 3013 CAGGCCTACAACCGGAGGCTGCTGCATAACATCCTTCCCAAGGACGTGGCGCCCCACTTC 3072

Qy 2881 CTGGCCCGGGAGCGCCGCAATGACAACGCGGGCACCCAAGATGCCCTGAATCAGCTGTGTGTGTT 2940
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Db 3073 CTGGCCCGGGAGCGCCGCCAACGAGCGTGTACTACCAATCCTGCGGAGTGCGCTGGCTGTC 3132

Qy 2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTCTATGTGGAGCAAACAATGAG 3000
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Db 3133 ATGTTTGCCTCCATCGCCAACTTCTCTGAGTTCTATGTGGACTGGAGCTGAGGGCGAACAATGAG 3192

Qy 3001 GGTGTCGAGTGCCTGCGCGCGCTGCTCAACGAGGATCATCGCTGACTTTGATGAGATTATCAGC 3060
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Db 3193 GGCGTGGAGTGCCTGCGCGCGCTGCTCAATGAGATCATCGCGGACTTTGATGAGATCATCAGT 3252

Qy 3061 GAGGAGCGGGTTCCGGCCAGCTGGAAAAGATCAAGACCAGATTGGTAGCACCTACATGGCTGCC 3120
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Db 3253 GAGGAGAGGTTCCGGGCAGCTGGAGAGAGATCAAGACCAAGCGGTGACACTTACATGGCCGCCC 3312

Qy 3121 TCAGGGCTGAACGCCAGCAGCACCTACGATGTGGGCCGCGCTCCCACATCACTGCCCCTGCT 3180
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Db 3313 TCCGGGCTAAATGCCAGCAGCACCTATGACCAGGTGCCCACATGCACCGCCCCTGCCA 3372

Qy 3181 GACTACGCCATGCGGCTTCATGCGGCTTATGGAGCAGATGAGCACATCAATGAGCACTCCTTCAACAAT 3240
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Qy 3241 TTCCAGATGAAGATTGGGCTGAACAATGGGCCAGTGTGGCTGGGGCTCGG 3300
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Db 3433 TTCCAGATGAAGATGATCGGGTTGAACATGGGTCCGGTTGTGCAGGGGTGTGGGGCCCGG 3492

Qy 3301 AAGCCACCAGTGATGATGACAATCTGGGGAACACAGTGAAATGTCTCTAGTGTCTGTAGCAGCACG 3360
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Qy 3421 TACCAGCTGGAGTGTGAGGGCACCTGGGATGTGCAAGGTGAAGGGGGAGATGACCACCTAC 3480
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Qy 3481 TTCCTCAATGGGCCCCCAGCAC--CACAAATTCAGCTGAAGGA 3538
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Db 3673 TTCCTCAATGGGCCCCAGCAGTTAGCAGAGGCCAGCAGTGGAAATTCAACCAAGGGA 3732

Qy 3539 CCAAGGTGGGCACT 3552

Qy 1381 GTACGTGAGGTGACAGGTGTGAAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1440
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Db 1573 GTGCGTGAGGTGAACGGGTGTAAATGTGAAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGTA 1632

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Db 1693 CTGGGCCAACCACCATGAGGAGGGGGGCCGGGCCGGCCGCATCCACATCACTCGGGCCACA 1752

Qy 1561 CTGCAGTACCTGAACGGGGACTACAGCGGTGAGCCAGGCCGTGGTGGCGAGCGCAACGCG 1620
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Qy 1621 TACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCTCGGCGCCCAGCCAGAAACGGAAA 1680
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Db 1813 TACCTCAAGGAGCAGTCAGTGCATTGAGACCTTCCTCATACTACGGAGCCCAGCCAGAAACGGAAA 1872

Qy 1681 GAGGAGAAGGCCATGTCTGGCCAAGCTGCAGCGGACTCGGCCAACTCCATGGAAGGCTG 1740
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Db 1873 GAGGAGAAGGCCATGTCTGGTCAAGCTGCAGCGGACGCGGCCAACTCCATGGAAGGACTG 1932

Qy 1741 ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCCGACCAAGGACTCCAAGGGCTTCCGC 1800
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Db 1933 ATGCCCTACAACCGGGCCTGGGTTCCTGACCGTGCCTTCTCCCCGACCAAGGACTCTAAGGCCATTCCGA 1992

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Qy 1921 CGGAAGGACCATGTGCGGCCGGTTTCTTGCTCACCTTCCAGAGAGGAGGATCTTGAGAAGAAG 1980
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Db 2173 TATTCACGGAAAGTAGACCCTCGTTTCGGAGCCTACGGTCTTGGGCCTCGTGTCCTGTTTTTC 2232

Qy 2041 TGCTTCATCTGCTTCCCAGCTTCATCTTCCCACATCACCCTGATGCTTGGGATC 2100
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RESULT 15
MUSADNLCYC
LOCUS       MUSADNLCYC             3465 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Mus musculus adenylyl cyclase type 6 mRNA, partial cds.
ACCESSION   M96653
VERSION     M96653.1  GI:191726
KEYWORDS    adenylyl cyclase type VI.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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REFERENCE   1  (bases 1 to 3465)
  AUTHORS   Premont,R.T.
  TITLE     Multiple mechanisms underlying desensitization of the liver
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  JOURNAL   Unpublished (1992)
REFERENCE   2  (bases 1 to 3465)
  AUTHORS   Premont,R.T., Jacobowitz,O. and Iyengar,R.
  TITLE     Lowered responsiveness of the catalyst of adenylyl cyclase to
            stimulation by GS in heterologous desensitization; a role for
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  JOURNAL   Endocrinology 131 (6), 2774-2784 (1992)
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ORIGIN

Query Match        78.4%;  Score 2785.2;  DB 10;  Length 3465;
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Job time : 12743 secs

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OM nucleic - nucleic search, using sw model

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Run on: January 7, 2004, 01:25:55 ; Search time 7020 Seconds
                                         (without alignments)
                              12297.649 Million cell updates/sec

Title: US-09-750-240-10
Perfect score: 3552
Sequence: 1 atgtcatgtcttagtggcct..........aagggaccaaggtgggcact 3552

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215223056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
          1: em_estba:*
          2: em_esthum:*
          3: em_estin:*
          4: em_estmu:*
          5: em_estcov:*
          6: em_estpl:*
          7: em_estro:*
          8: em_htc:*
          9: gb_est1:*
         10: gb_est2:*
         11: gb_htc:*
         12: gb_est3:*
         13: gb_est4:*
         14: gb_est5:*
         15: em_estfun:*
         16: em_estom:*
         17: em_gss_hum:*
         18: em_gss_inv:*
         19: em_gss_pln:*
         20: em_gss_vrt:*
         21: em_gss_fun:*
         22: em_gss_mam:*
         23: em_gss_mus:*
         24: em_gss_pro:*
         25: em_gss_rod:*
         26: em_gss_phg:*
         27: em_gss_vrl:*
         28: gb_gss1:*
         29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	820	23.1	1039	12	BM811640	BM811640 AGENCOURT
2	812	22.9	895	14	CA487177	CA487177 AGENCOURT
3	786.6	22.1	1016	13	BQ081496	BQ081496 AGENCOURT
4	747.4	21.0	872	14	CA453976	CA453976 AGENCOURT

5	726.8	20.5	775	10	BF792125	BF792125	BF792125	602252571
6	723	20.4	986	13	BU161782	BU161782	BU161782	AGENCOURT
7	660.4	18.6	710	2	HSM071986	Bx481818	Homo sapi	
8	657.8	18.5	834	13	BX355179	BX355179	BX355179	BX355179
9	621.2	17.5	757	14	CA511319	CA511319	CA511319	UI-R-FJ0-
10	613.8	17.3	878	14	CA487529	CA487529	CA487529	AGENCOURT
11	607.8	17.1	676	10	BB840188	BB840188	BB840188	QV0-FN018
12	601	16.9	740	13	BU611374	BU611374	BU611374	UI-M-FI0-
13	583.4	16.4	711	14	CB247656	CB247656	CB247656	UI-M-FI0-
14	578.4	16.3	1225	12	BI691747	BI691747	BI691747	603307455
15	570.6	16.1	1043	10	GG297229	GG297229	GG297229	602394937
16	569.4	16.1	743	12	BI685206	BI685206	BI685206	603310213
17	568	16.0	889	13	BX451612	BX451612	BX451612	BX451612
18	551.4	15.5	581	12	BG993320	BG993320	BG993320	MR3-HT099
19	551.2	15.5	796	10	BG287169	BG287169	BG287169	602381888
20	542	15.3	790	12	BI255147	BI255147	BI255147	60297410
21	537	15.1	537	2	HSM095228	Bx501511	Homo sapi	
22	532.4	15.0	890	13	BU187098	BU187098	BU187098	AGENCOURT
23	525.2	14.8	894	14	CA488920	CA488920	CA488920	AGENCOURT
24	517.6	14.6	819	13	BU111903	BU111903	BU111903	603126114
25	512.4	14.4	905	13	BQ231940	BQ231940	BQ231940	AGENCOURT
26	510.8	14.4	3340	11	CNSLT117U	CNSLT117U	BX248285	human ful
27	498	14.0	607	12	BM943080	BM943080	BM943080	UI-M-CG0p
28	487	13.7	487	9	AL119686	AL119686	AL119686	DKFZp761N
29	485.8	13.7	565	12	BG872335	BG872335	BG872335	60279261b
30	477.6	13.4	501	13	BX474447	BX474447	BX474447	DKFZp6860
31	474.8	13.4	652	9	AA207907	AA207907	AA207907	mv84h06.r
32	464.8	13.1	525	12	BM090325	BM090325	BM090325	505523 MA
33	459.2	12.9	737	10	BB377119	BB377119	BB377119	601229307
34	456	12.8	899	13	BX420266	BX420266	BX420266	601229307
35	451.2	12.7	685	12	BM964004	BM964004	BM964004	UI-M-EQ0-
36	442.6	12.5	809	9	AU169950	AU169950	AU169950	AU169950
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39	407.4	11.5	420	10	BF935972	BF935972	BF935972	IL2-NT019
40	405.6	11.4	453	10	BB838164	BB838164	BB838164	CM1-FN010
41	405	11.4	691	14	CD217903	CD217903	CD217903	pgrin.pk0
42	402.8	11.3	442	9	AI905602	AI905602	AI905602	CM-BT094-
43	402.8	11.3	466	9	AI905641	AI905641	AI905641	CM-BT094-
44	401	11.3	496	10	BF653668	BF653668	BF653668	277573 MA
45	400.8	11.3	447	10	BE487801	BE487801	BE487801	176908 BA

ALIGNMENTS

RESULT 1
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LOCUS   BM811640   AGENCOURT 6489534 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724057
                        5', mRNA sequence.   1039 bp   mRNA   linear   EST 05-MAR-2002
DEFINITION BM811640   AGENCOURT 6489534 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724057
                        5', mRNA sequence.
ACCESSION   BM811640
VERSION   BM811640.1 GI:1912B463
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1039)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12712 row: 1 column: 10
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5724057"
                     /lab_host="DH10B"
                     /clone_lib="NIH MGC 125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
BASE COUNT     204 a   302 c   262 g   269 t   2 others
ORIGIN

Query Match    23.1%;    Score 820;  DB 12;  Length 1039;
Best Local Similarity  98.0%;  Pred. No. 1.3e-165;
Matches 840;  Conservative 0;  Mismatches 16;  Indels 1;  Gaps 1;

Qy   2112 CTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTTCCTGTGTTCTCTGTT 2171
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Db      1 CTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTTCCTGTGTTCTCTGTT 60

Qy   2172 CCCTAAGGCCCTGCAACGTCTGTCCCCGCAGCATTGTCCGCTCACGGGCACATAGACCGC 2231
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Db     61 CCCTAAGGCCCTGCAACGTCTGTCCCCGCAGCATTGTCCGCTCACGGGCACATAGACCGC 120

Qy   2232 AGTTGGCATCTTTCCGTCCTGCTGTTGTTACTTCTGCCATTGCCAACATGTTCACCTG 2291
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Qy   2292 TAACCACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGACAT 2351
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Db    181 TAACCACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGACAT 240

Qy   2352 CACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCGTGTGA 2411
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Qy   2412 GGGCACCACCATGCCCAGCTTTCCTGAGTACTTCATCGGGAACACATGTGCTGAGTCT 2471
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Db    301 GGGCACCACCATGCCCAGCTTTCCTGAGTACTTCATCGGGAACACATGTGCTGAGTCT 360

Qy   2472 CTTGGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATGATCTTTGT 2531
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Qy   2532 CTTGGGGCTCATCTATTTGGTGCTGCTGCTTCTGCTGGGTCCCCCAGCCACCATCTTTGACAA 2591
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Qy   2592 CTATGACCTACTGCTTGGGCGTCCATGGCGTCCTGGCTTCTTCCAATGAGACCTTTGATGGGCT 2651
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Qy   2652 GGACTGTCCAGCTGCGAGGAGGTGGCCCTCAAATATATGACCCCGTGATTCTGCTGGT 2711
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Qy   2712 GTTTGGGCTGGCGCTGTATCTGCATGCTGCAGCGGTGGAGTGCAGCGTCGACTGCGCCGCCTAGACTT 2771
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Qy   2892 GGCGCCGCAATGATGAACTCACTACTATCAGTCGTGTGAGTGTGTG-GCTGTTATGTTGCCT 2950
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Db    781 GCGCCCCGCCATGATGAACTCACTACTATCAGTCGTGTGAGTGTGGCGGCTGTTATGTTTGCCT 840

Qy   2951 CCATTGCCAACTTCTCT 2967
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RESULT 2
CA487177
LOCUS       CA487177  AGENCOURT 10809523 MAPcL Homo sapiens cDNA clone IMAGE:6718209 5',
            mRNA sequence.
DEFINITION  CA487177             895 bp    mRNA    linear    EST  14-NOV-2002
ACCESSION   CA487177
VERSION     CA487177.1  GI:24945990
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14274 row: c column: 09
            High quality sequence stop: 669.
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                     LNCaP"
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                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
BASE COUNT     182 a   242 c   258 g   212 t   1 others
ORIGIN

Query Match    22.9%;    Score 812;  DB 14;  Length 895;
Best Local Similarity  98.9%;  Pred. No. 6.4e-164;
Matches 870;  Conservative 0;  Mismatches 5;  Indels 5;  Gaps 5;

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Qy   2458 ATGCTGCTGAGTCTCTTGGCCAGCTCTTCCTGCACATCAGCAGCATCAGCAGGTTG 2517
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Qy   2518 GCCATGATCTTTGTCTTGTGGGCTCATCTATTTGGTGTGCTTCTGCTGGGTCCCCCAGCC 2577
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Qy  2578 ACCATCTTTGACAACTATGACCTACTGCTTGCGCTGGCGTCCATGGCTTGGCTTCTTCCAATGAG 2637
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Qy  2638 ACCTTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCT 2697
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Qy  2758 GCCCGCCTAGACTTCCTCTGGAAACTACAGGGCAACAGGGAGAGGAGGAGGATGGAGGAG 2817
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Qy  2998 GAGGGGTGTCGAGTGCCTGCGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATC 3057
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Db   601 GAGGGGTGTCGAGTGCCTGCGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATC 660

Qy  3058 AGCGAGGAGGGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCT 3117
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13567   row: f   column: 20
High quality sequence start: 31
High quality sequence stop: 645.

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                /tissue_type="dorsal root ganglia"
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                /clone_lib="Lupski dorsal root ganglion"
                /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:
                5'-TCGACCACGCGTCCG-3' and
                5'-GACTAGTTCTGATCGCAGGCGGCCGCCCT(15)-3'. Size selected >
                1 kb for average insert length 1.7 kb. This is a primary
                library, non-amplified. Library constructed by Life
                Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                College of Medicine) and is available through Life
                Technologies."
BASE COUNT      186 a      297 c      268 g      265 t
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Query Match   22.1%;   Score 786.6; DB 13;   Length 1016;
Best Local Similarity 94.7%; Pred. No. 1.9e-158;
Matches 912; Conservative 0; Mismatches 39; Indels 12; Gaps 9;

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Qy  2129 TCACCGTGCTGATCTGTGCTGTGTGTGTTCTCGTGTTCCTGGTGTTCCTGTCCTGCGCCTGCAAC 2188
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Qy  2189 GTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCG 2248
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Qy  2309 GGAGCGTGCGAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCTGACCTGC 2368
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Qy  2369 AGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCGTGTGAGGGCACCATGCCCACCT 2428
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Qy  2429 GCAGCTTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTGTCT 2488
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   522 TGGTGCTGCTTCGTGCTGCTCGTGGGTCCCCCAGCCACCACCATCTTTGACAACTATGACCTACTGCTTG 581

Qy  2609 GGGTACCATGCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGCAG 2668
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 3
BQ881496
```
LOCUS       BQ881496               1016 bp    mRNA    linear    EST 16-AUG-2002
DEFINITION  AGENCOURT_8229097 Lupski dorsal root ganglion Homo sapiens cDNA
            clone IMAGE:6182035 5', mRNA sequence.
ACCESSION   BQ881496
VERSION     BQ881496.1  GI:22273504
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1016)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
Db   582  GGGTCCATGGCTTGGCTTCTT-CAATGAGACCCTTTGATGGGCTGGACTGTCCAGCTGCAG 640
               |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Qy  2669  GGAGGGT-GGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTGCCGCTGGCGCTG 2727

Db   641  GGAGGGGTGGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTGCCGCTGGCGCTG 700

Qy  2728  TATCTGCATGCTCAGCAGGTGGAGTGCACTG-CCCGCCTAGACTTCCTCTGGAAACTACA 2786
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   701  TATCTGCATGCTCAGCAGGTGGAGTGCACTGCCCCGCCCTAGACTTCCTCTGGAAACTACA 760

Qy  2787  GGCAACAGGGGAGGAAGAGGAGATG-AGGAGCTACAGGCATACAACCGAGACTGTCTGC 2845
               ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   761  GGCAACAGGGGAGGAAGAGGAGATGGAGGAGCTACAGGCATACAAACGAGAGCTGTCTGC 820

Qy  2846  ATAACATTCTGCCCAAGGACGACCGGCCGCCCACTTCCTGG--CCCGGGAGCCGCCGCAATGA 2903
               |||||||||||||||||||||||||||||||||||||||  |||| ||||||||||||
Db   821  ATAACATTCTGCCCAAGGACGACCGGCCGCCCCCCTTTTCTGGGGAACGGCCGCCCAATGA 880

Qy  2904  TGAACTTCTACTATCAGTC---GTGTGAGTGTGTGGCGTGTATGTTGCCTCCATT-GCCA 2959
               |||||||||||||||||   |||| ||| ||||||||  |||||||| || ||||
Db   881  TGGACTTCTACTATCAATCCTTGTGAGTGGTGTGTTATGGTTGGTTGGCCTCCATTGGCCA 940

Qy  2960  ACTTCTCTGAGTTCTAT-GTGGAGCTGGAGGCAAACAATG-AGGGTGTCGAGTGCCTGCG 3017
               |||||||||||||||| ||||| |||||||||||||||  ||||||||||||||||||
Db   941  CCTTCTCTGAGTTCCATGGGGGAGCTGGACGGAGAAACAATGAAAGGGGTCCAAGGCCTGCG 1000

Qy  3018  GCT 3020
              |  |
Db  1001  GTT 1003
```

RESULT 4

```
CA453976
LOCUS       CA453976              872 bp    mRNA     linear   EST 12-NOV-2002
DEFINITION  AGENCOURT 10738556 MAPcL Homo sapiens cDNA clone IMAGE:6718625 5',
            mRNA sequence.
ACCESSION   CA453976
VERSION     CA453976.1  GI:24903260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 872)
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14275 row: d  column: 17
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
     source          1..872
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6718625"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                     LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
```

· Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

```
BASE COUNT    153 a    271 c    228 g    220 t
ORIGIN
```

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Query Match      21.0%;   Score 747.4;  DB 14;  Length 872;
Best Local Similarity  99.9%;  Pred. No. 5e-150;
Matches  748;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
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Qy  1690  GCCATGTCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGC 1749
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  GCCATGTCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGC 60

Qy  1750  TGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGCCTTCCAAGGCCTTCCGCCAGATGGGC 1809
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGCCTTCCAAGGCCTTCCGCCAGATGGGC 120

Qy  1810  ATTGATGATTCAGCAAAGACAACACCGGGGCACCCAAGATGCCCGAGCATTGATCAGTCTGCGGGAGGATGAG 1869
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ATTGATGATTCAGCAAAGACAACAACCGGGGCACCCAAGATGCCCGAGCATTGATCAGTCTGCGGGAGGATGAG 180

Qy  1870  GTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATGCGCGCAGCGAAGAC 1929
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATGCGCGCAGCGAAGAC 240

Qy  1930  CATGTGCGCCGGTTTCGGGAGCCTAGTTGCCTGTGGTCTTCTGTTGTTCTGCTTCATC 1989
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CATGTGCGCCGGTTTCGGGAGCCTAGTTGCCTGTGGTCTTCTGTTGTTCTGCTTCATC 300

Qy  1990  AAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCCTGGTCTTGGTCTTCGGAGCCTACGTTGCC 2049
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCCTGGTCTTGGTCTTCGGAGCCTACGTTGCC 360

Qy  2050  TGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCGATGCTTGGGATCTATGCCAGC 2109
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  TGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCGATGCTTGGGATCTATGCCAGC 420

Qy  2110  ATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGGTTTATGTTGTGTTTCTGTTGTTCTCTG 2169
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGGTTTATGTTGTGTTTCTGTTGTTCTCTG 480

Qy  2170  TTCCCTAAGGCCCTGCAACGTCGTCCCGCCGCAGCATTGTCCGCTCACGGGCACATAGCACC 2229
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTCCCTAAGGCCCTGCAACGTCGTCCCGCCGCAGCATTGTCCGCTCACGGGCACATAGCACC 540

Qy  2230  GCAGTTGGCATCTTTTCTGCTGTTGTTTACTTCTGCCATTGCCAAACATGTTCACC 2289
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Db   541  GCAGTTGGCATCTTTTCTGCTGTTGTTTACTTCTGCCATTGCCAAACATGTTCACC 600

Qy  2290  TGTAACCACACCCCCATAGGAGCTGTGCAGCCCGGATGCTGAATTAACACCTGCTGAC 2349
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGTAACCACACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTAACACCTGCTGAC 660

Qy  2350  ATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCCTGTGT 2409
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Db   661  ATCACTGCCTGCCACCTGCAGCTCAATTACTCTCTGGGCCTGGATGCTCCCCCTGTGT 720

Qy  2410  GAGGGCACCATGCCCACCTGCAGCTTTCC 2438
               |||||||||||||||||||||||||||||
Db   721  GAGGGCACCATGCCCACCTGCAGCTTTTC 749
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RESULT 5

```
BF792125
LOCUS       BF792125              775 bp    mRNA     linear   EST 12-JAN-2001
DEFINITION  602252571F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345144 5',
            mRNA sequence.
ACCESSION   BF792125
VERSION     BF792125.1  GI:12097179
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
Qy   3286  GTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGT  3345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551  GTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGT  610

Qy   3346  CGTATGGACAGCACGGGGGTCCCGACCGGGGTCCCGACCGGTGTACCAGGTT  3405
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Db    611  CGTATGGACAGCACGGGGGTCCCGACCGGGGTCCCGACCGGTGTACCAGGTT  670

Qy   3406  CTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGAGGGGTGTCAAGTGAAGGGCAAGGGG  3465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671  CTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGAGGGGTGTCCACGTGAAGGGCAAGGGG  730

Qy   3466  GAGATGACCACCTACTTCCTCAATGGGGGCCC  3497
           ||||||||||||||||||||||||||||||||
Db    731  GAGATGACACCTAA--TTCTCAATGGGGGCCC  760
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RESULT 6
BU161782
LOCUS   BU161782   986 bp   mRNA   linear   EST 04-SEP-2002
DEFINITION   AGENCOURT_7968019 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6170500
              5', mRNA sequence.
ACCESSION   BU161782
VERSION   BU161782.1 GI:22675692
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 986)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13537 row: f column: 05
              High quality sequence stop: 623.
FEATURES   Location/Qualifiers
     source   1..986
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6170500"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."
BASE COUNT   206 a   292 c   246 g   242 t
ORIGIN

Query Match   20.4%; Score 723; DB 13; Length 986;
Best Local Similarity 97.3%; Pred. No. 9e-145;
Matches 746; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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Qy   2050  TGCTTCATCCAGCTTCCATCTTCCCACACTCCACCCTGGGATCGATGCTTGGGATCTATGCCAGC  2109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TGCTTCATCCAGCTTCCATCTTCCCACACTCCACCCTGGGATCGATGCTTGGGATCTATGCCAGC  60

Qy   2110  ATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTGTGTACTCCCTGTGGTTCTCTG  2169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTGTGTACTCCCTGTGGTTCTCTG  120
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REFERENCE   1 (bases 1 to 775)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM9964 row: m column: 17
              High quality sequence stop: 711.
FEATURES   Location/Qualifiers
     source   1..775
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4345144"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_84"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT   184 a   199 c   239 g   153 t
ORIGIN

Query Match   20.5%; Score 726.8; DB 10; Length 775;
Best Local Similarity 98.8%; Pred. No. 1.3e-145;
Matches 743; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

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Qy   2746  GTGGAGTCGACTGCCGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGGGAGAAGGAG  2805
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11  GTGGAGTCGACTGCCGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGGGAGAAGGAG  70

Qy   2806  GAGATGAGGAGAGCTACAGGCGATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGAC  2865
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71  GAGATGAGGAGAGCTACAGGCGATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGAC  130

Qy   2866  GTGGCGGCCCACTTCCTGCCCCGGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGT  2925
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Db    131  GTGGCGGCCCACTTCCTGCCCCGGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGT  190

Qy   2926  GAGGTGTGTGGCTGTTATGTTGCCTCCAACTTCTCTGAGTTCTCTATGTGGAGCTG  2985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191  GAGGTGTGTGGCTGTTATGTTGCCTCCAACTTCTCTGAGTTCTCTATGTGGAGCTG  250

Qy   2986  GAGGCAAACAATGAGGGTGTCGAGTGCCTCGGCTGTGCTCAACGAGATCATCGCTGACTTT  3045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251  GAGGCAAACAATGAGGGTGTCGAGTGCCTCGGCTGTGCTCAACGAGATCATCGCTGACTTT  310

Qy   3046  GATGAGATTATCAGCGAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGC  3105
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Db    311  GATGAGATTATCAGCGAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGC  370

Qy   3106  ACCTACATGGCTGCCTCAGGGCTGAACGCCACCTACGATCAGGTGGGCCGCTCCCAC  3165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371  ACCTACATGGCTGCCTCAGGGCTGAACGCCACCTACGATCAGGTGGGCCGCTCCCAC  430

Qy   3166  ATCACTGCCCTGGCTGACTACGGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAG  3225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431  ATCACTGCCCTGGCTGACTACGGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAG  490

Qy   3226  CACTCCTTCAACAATTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGT  3285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491  CACTCCTTCAACAATTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGGCAGGT  550
```

CC   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC   Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC   sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
CC   consortium of the German Genome Project.
CC   No 81 sequence available.
CC   This clone (DKFZp686L20227) is available at the RZPD in Berlin.
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC   14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key   Location/Qualifiers
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FT   source   1..710
FT   /db_xref="taxon:9606"
FT   /mol_type="mRNA"
FT   /organism="Homo sapiens"
FT   /clone="DKFZp686L20227"
FT   /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
FT   DH10B; Sites SfiIA + SfiIB"
FT   /dev_stage="adult"
FT   /tissue_type="cDNA-collection"
XX
SQ   Sequence 710 BP; 132 A; 227 C; 178 G; 170 T; 3 other;

Query Match   18.6%;   Score 660.4; DB 2; Length 710;
Best Local Similarity 99.1%; Pred. No. 2.4e-131;
Matches 683; Conservative   0; Mismatches   4; Indels   4; Gaps   2;

Qy 1697 TGGCCAAGCTGCAGCGGACTCGGCCAACTCCATGGAAGGCTGATGCCGGCCGCTGGGTTC 1756
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   24 TGGCCAAGCTGCAGCGGACTCGGCCAACTCCATGGAAGGCTGATGCCGGCCGCTGGG-TC 82

Qy 1757 CTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCCTTCCGCAGATGGGCATTGATG 1816
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 CTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCCTTCCGCAGATGGGCATTGATG 142

Qy 1817 ATTCCAGCAAAGACACCGGGACACCGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATG 1876
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 ATTCCAGCAAAGACACCGGGACACCGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATG 202

Qy 1877 AGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGCGGAAGGACCATGTGC 1936
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203 AGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGCGGAAGGACCATGTGC 262

Qy 1937 GCCGGTTTCTGCTCACCTTCACCTTCACCAGAGAGAGATCTTGAGAAGAAGTACTCCCGGAAGGTGG 1996
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   263 GCCGGTTTCTGCTCACCTTCACCTTCACCAGAGAGAGATCTTGAGAAGAAGTACTCCCGGAAGGTGG 322

Qy 1997 ATCCCCGCTTCGGAGCCTACGTCGTCCCGGCCTAGCGCTTCGTGTGCCCTGTTGGTCTTCTGCTTCATCGCCTTCCAGCATCTTCC 2056
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323 ATCCCCGCTTCGGAGCCTACGTCGTCCCGGCCTAGCGCTTCGTGTGCCCTGTTGGTCTTCTGCTTCATCGCCTTCCAGCATCTTCC 382

Qy 2057 TCCAGCTTCTCATCTTCCCCACACTCACCCCTGATGCTTGGGATCATGCTTGGGATCATGCTTGGGATCATCTTCC 2116
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Db   383 TCCAGCTTCTCATCTTCCCCACACTCACCCCTGATGCTTGGGATCATGCTTGGGATCATCTTCC 442

Qy 2117 TGCTGCTGCTAATCACCGTGCTGATCTGTGTGTCGTGTACTCCTGGTTCTCTGTTCCTA 2176
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Db   443 TGCTGCTGCTAATCACCGTGCTGATCTGTGTGTCGTGTACTCCTGGTTCTCTGTTCCCTA 502

Qy 2177 AGGCCCTGCAACGTCTGTCCCGCAGCAGCATTGTCCCGCCGCTCACGGGCCACATAGCAGTG 2236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 AGGCCCTGCAACGTCTGTCCCGCAGCAGCATTGTCCCGCCGCTCACGGGCCACATAGCAGTG 562

Qy 2237 GCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACC 2296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 GCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGTNACTTCTGCCATTGCCAACATGTTCACCTGTAACC 622

Qy 2297 ACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTG 2356
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   623 ACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGCANGCCGGATGCTGAANTTAACA-CTGCTGACATCACTG 681

Qy 2357 CCTGCCACCTGCAGCAGCTCAATTACTCT 2385
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Db

RESULT 7
HSM071986
ID   HSM071986 standard; RNA; EST; 710 BP.
XX
AC   BX481818;
XX
SV   BX481818.1
XX
DT   09-MAY-2003 (Rel. 75, Created)
DT   09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp686L20227_r1 (from clone DKFZp686L20227)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-710
RA   Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RT   ;
RL   Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX
CC   This is the 5' sequence of the clone insert

Qy 2170 TTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCAGCATTGTCCCGCCGCAGCACATAGCACC 2229
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCAGCATTGTCCCGCCGCAGCACATAGCACC 180

Qy 2230 GCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACC 2289
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACC 240

Qy 2290 TGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTAACACCTGCTGAC 2349
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGTAACCACACCCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTAACACCTGCTGAC 300

Qy 2350 ATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTTGGATGCTCCCCTGTGT 2409
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTTGGATGCTCCCCTGTGT 360

Qy 2410 GAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGT 2469
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGT 420

Qy 2470 CTCTTGGCCAGCTGCTCTTCTCCGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTT 2529
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTCTTGGCCAGCTGCTCTTCTCCGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTT 480

Qy 2530 GTCTTGGGGCTCATCTATTTGGTGCGCTTCGTCGTGGGTCCCCCAGCCACCATCTTTGAC 2589
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTCTTGGGGCTCATCTATTTGGTGCGCTTCGTCGTGGGTCCCCCAGCCACCATCTTTGAC 540

Qy 2590 AACTATGACCTACTGCTTGGCGTCCATGGGTCGGCTTCTTCCAATGAGACCTTTGATGGG 2649
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AACTATGACCTACTGCTTGGCGTCCATGGGTCGGCTTCTTCCAATGAGACCTTTGATGGG 600

Qy 2650 CTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTG 2709
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTG 660

Qy 2710 GTGTTTCGCGTGGCGCTGTATCTGCA-TGCTCAGCAGGTGGAGTCCACTGCCCGCCTAGA 2768
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Db   661 GTGTTTCGCGTGGCGCTGTATCTGCACCCAAGGGGATGCGACTGCCCGCCTAAA 720

Qy 2769 CTTCCTCTGGAAACTACAGGCAACAGGGGACAGGGAGGAGGATGGAGG 2815
         |||||||||||||||||||||||||||||||||||||||
Db   721 CTTCCCCTGGGAACTAAAGGCAACACGGGGAAAAGGAGGGAGGAGGATAATCG 767

Db   682 CCTGCCACCTGCAGCCAGCTCAATTACTCT 710

RESULT 8
BX355179
LOCUS   BX355179   834 bp   mRNA   linear   EST 05-MAY-2003
DEFINITION   BX355179 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
              cDNA clone CS0DD002YM08 5-PRIME, mRNA sequence.
ACCESSION   BX355179
VERSION   BX355179.1 GI:30377950
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 834)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 6892.f For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster/cgi?seq=CS0DD002BG04QP1&cluster=6892. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fullength.invitrogen.com/ InVitroGen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DD002BG04QP1.
FEATURES   Location/Qualifiers
     source   1..834
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DD002YM08"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   161 a   207 c   254 g   147 t   65 others
ORIGIN

Query Match   18.5%;   Score 657.8; DB 13; Length 834;
Best Local Similarity   86.8%;   Pred. No. 9.1e-131;
Matches 697; Conservative 64; Mismatches 37; Indels 5; Gaps 5;

Qy 1165 ACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTT 1224
         |||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Db   34 AGCAGGCTGGTACCGGTCCGGAATTCCCGGGATCTGGTCATGACCCTGAATGAGCTCTTT 93

Qy 1225 GCCCGGTTTGACAAGCTGGCTCGCGCGCTGCCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGGAC 1284
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||-
Db   94 GCCCGGTTTGACAAGCTGGCTCGCGCGCTGCCTGAGGRTCAAGATCTTGGGGGGC 153

Qy 1285 TGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGGGCCCGACCATGCCCACTGCTGTGTG 1344
         ||||||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||
Db   154 TGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGGGCCCCATGCCCMCTGCTGTGTG 213

Qy 1345 GAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAAT 1404
         ||||||||||||||||||||||||||||| ||||||| |||||||||||||||||||
Db   214 GGGATGGGGTRGACATGATTGAGGCCMTCYCSCTGGTACGTGAGGGGGACAGGTGTGAAT 273

Qy 1405 GTGAACATGCGCGTGGGCATCCACAGC-GGGCGCCTGCACTGCGGCGTCCTTGGCTTGCG 1463
         ||||||||||||:|||||||||||:::|||||||||||:||||||:|||:||||||:||::|
Db   274 KTKAACATGCGCGTGGGGSWTCCACAGCGGGCGCCTGMCYGCGCGGTCCYTKGCTTKCS 333

Qy 1464 GAAATGGCAGTTCAGTTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGG 1523
         |:||:||||:||||||||::||||||||||:|||||||||||||::|||:|::|:|:
Db   334 GRAATDGCMRTTCCATGTGTGGTCCCATGATGTGACCCYGGCGCCMAMCMCATGGRGGSMGG 393

Qy 1524 A-GGCGGGCTGGCCGTCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACT 1582
         : || |||| |||||||||||||||||||||||||| |||:||||||||||||:|||||:|
Db   394 RGGGCGGGCTGGGCGTCATCCACATCACTCGGGCAACACTGCMGTACCTGAACGGGGRCT 453

Qy 1583 ACGAGGTGGAGCCAGGCCGTGGTGCGGAGCGGCAACGCGGTACCTCAAGGAGCAGCACATTG 1642
         |||||||||||||||:|||||||||||||||:|||:|||:|:||||||||||||||||:
Db   454 ACGARGTGGAGCCAAGCCSGTGCGAGCGCMAMGTGTACCTCAAAGAGCMGCMCATTG 513

Qy 1643 AGACTTTCCTCATCCTGCGCGCGCCCAGCAGCAAACGAAAGAGGAGAAGAGGCCATGCTGGCCA 1702
         ||||||||||||||::||||||||| | |:|||||||||||||||||||||||||||||||||
Db   514 AGACTTTCCTCMTCCTGGGCGCCA-CAAAAAMGAAAARGAGAGGGCCATGCTGGCCA 572

Qy 1703 AGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCCGCGTCGGTTCCTGATC 1762
         ||:|||||||||||:||||||||||||||||||||||||||||||||||||:|
Db   573 ARCTKCAGCGGACTCGGGCCMACTCCMWRGAARGGCTGATGCCCGCGTCGGTTCCTGATC 632

Qy 1763 GTGCCTTCTCCCGGACCAAGGACTTCCAGGCCTTCCGCCAGATGGGCCATTGATGATTCCA 1822
         ||||||||||||||||||||||||:|||||||||||||| :|||:||||||:|||||||||
Db   633 GTGCCTTCTCCCGGACCAAAGACTTCCAAGGMCTWMCGCCAAAWGGGCCATWGATGWTTCCM 692

Qy 1823 GCAAAGACAACCGGGCACCCAGATGCCCAGATGCCCTGAACCCTGAGGATGGAGGTGGATGAGTTCC 1882
         ||:::|||:|||||||||| ||:|||:|||||||||||||||||||||||||||:|||||||:
Db   693 GMAAARACAAMCGGGGCMCCC-AGATGCCCTGAGGACCCTGAGGATGGATGGTGGATGAGTRYC 751

Qy 1883 TGAGCGTGCCATGATGCCCGCAGCATTGATCAGCTGCGG-AAGGACCATGTGCGCCGG 1941
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Db   752 TGAGMCGTGCMAWCGATGCCCGCAGCATTGATCARCTGCGGAAAGAACAAWRTGCGCCCGG 811

Qy 1942 TTTCTGCTCACCTTCCAGAGAGA 1964
         |||||:||||:|||||||||||||
Db   812 TTTCTGCTCMCCTTCCAAAGAGA 834

RESULT 9
CA511319
LOCUS   CA511319   757 bp   mRNA   linear   EST 15-NOV-2002
DEFINITION   UI-R-FJ0-cpw-m-04-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone
              UI-R-FJ0-cpw-m-04-0-UI 5', mRNA sequence.
ACCESSION   CA511319
VERSION   CA511319.1 GI:25002273
KEYWORDS   EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE   1 (bases 1 to 757)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED   8889548
COMMENT   Contact: Soares, MB
              Coordinated Laboratory for Computational Genomics
              University of Iowa
              375 Newton Road, 4156 MBRF, Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: bento-soares@uiowa.edu
              Tissue Procurement: Dr. James Lin, University of Iowa
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Researchers may obtain clones from Research
              Genetics (www.resgen.com).
              Seq primer: M13 REVERSE.
FEATURES   Location/Qualifiers
     source   1..757
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"

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Db      661 CTAGCTGCCAAGGGCTACCAACTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGAAGGGG 720
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Qy     3466 GAGATGACCACCTACTTCCTCAATGGGGCCCCAGCAG 3503
            ||||||||||||| ||||||||||||||||||||
Db      721 GAGATGA-CACCTACTTCCTCAATGGGGCCCCAGCAG 757

RESULT 10
CA487529
LOCUS       CA487529
DEFINITION  AGENCOURT_10808594 MAPcL Homo sapiens cDNA clone IMAGE:6719019 5',
            mRNA sequence.
ACCESSION   CA487529
VERSION     CA487529.1  GI:2947128
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement:Kristi A. Egland, Ira Pastan
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14276 row: e  column: 03
            High quality sequence stop: 484.
FEATURES             Location/Qualifiers
     source          1..878
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719019"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                     , LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee & Ira Pastan: Discovery of new breast
                     cancer genes encoding membrane and secreted proteins.
                     Manuscript submitted."
BASE COUNT      201 a    234 c    273 g    170 t
ORIGIN

Query Match             17.3%;  Score 613.8;  DB 14;  Length 878;
Best Local Similarity   98.5%;  Pred. No. 2.6e-121;
Matches  641;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    2;

Qy      828 GCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTT 887
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCAGCTCGGTGCCAATGTGCTGCTGTT 60

Qy      888 CCTCTGCACCAACGTCATTGGCATCTGGGGACACCAGTGAATGTCTCTAGT 947
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCTCTGCACCAACGTCATTGGCATCTGGGGAAACACGGTGAATGTTTCCAGC 120

Qy      948 GGCCTTTCAGGAGACCCGGTTACATCCAGGCCCGGCTCCACCTGCCGCAGAATCG 1007
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGCCTTTCAGGAGACCCGGTTACATCCAGGCCCGGCTCCACCTGCCGCAGAATCG 180

Qy     1008 GCAGCAGGAGCGGCGCTGCTCGTCGGTATTGCCCAGCACGTTGCCATGGAGATGAAAGA 1067
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Db      182 a    201 c    229 g    145 t
BASE COUNT
ORIGIN

Query Match             17.5%;  Score 621.2;  DB 14;  Length 757;
Best Local Similarity   89.6%;  Pred. No. 6.6e-123;
Matches  679;  Conservative    0;  Mismatches   78;  Indels    1;  Gaps    1;

Qy     2746 GTGGAGTCGACTGCCCGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAG 2805
            |||||| ||||||| ||| ||||||||||||||| |||||||||||||||||| |||||||
Db        1 GTGGAATCACCGCCCCCTGGACTTTCCTGTGGAAACTGCAGGCCCAGGGGAGAGGAGGAG 60

Qy     2806 GAGATGGAGGAGCTACAGGCATACACCGGAGGGCGTCGCTGCGATAACATTCGCCCAAGGAC 2865
            |||||||||||||| || |||  ||||||||||||||||||||||||| ||| |||||||||
Db       61 GAGATGGAGAGTTGCAGGCGCTACAACCGGGCGGCTGCTACAACATCCTTCCCAAGGAC 120

Qy     2866 GTGGCGCCCACTTCCTGGCCCGGAGCGACGGCCCAATGATGAACTCTACTATCAGTCGTGT 2925
            |||||||||||||||| ||||||||||||||| |||||| ||||  ||||||||||||| |
Db      121 GTGGCTGCCCACTTCCTGGCCCGGAGCGATGGCCGCGCCAACGAGTGTACTACCAATCCTGC 180

Qy     2926 GAGTGTGTGGCTGTTATGTTTGCCTCCAACTTCTCTGAGTTCATGTGAGCTG 2985
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Db      181 GAGTGCGTGGCTGTCATGTTTGCCTCCAACTTCTCTGAGTTCTATGTGGAACTG 240

Qy     2986 GAGGCAAACAATGAGGGTGTCGATGGCTGCTGGCGTGCTCGGCAACGAGATCATCGCTGACTTT 3045
            |||| |||||||||||||| ||||||||||||||||||| ||||  |||||||||||||||||
Db      241 GAGGCGAACAATGAGGGTGCTGAGTGGCCTGCGACTGCTCCAATGAGATCATCGCGGACTTT 300

Qy     3046 GATGAGATTATCAGCGAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGC 3105
            |||||||||||||||| |  |||||||||||||||||||||||||||||||||||||||||
Db      301 GATGAGATCATCAGTGAGGAGGAGTTCCGGCAGCTGGAGAAGATCAAGACCATCGGTAGC 360

Qy     3106 ACCTACATGGCTGCCTCAGGGCTGACACGCACCTACGAGACGAGCACCAGCTCGGCGGCCGTCTCCCAC 3165
            | |||||||| || ||| |||  |||||| ||| ||||| ||| |||| |||||||||||||||||||
Db      361 ACTTACATGGGCGCCTCAGGGCTAAAATGGGCCTATGCAGAAACACATCAACGAC 420

Qy     3166 ATCACTGCCCTGGCTACACGCCGGGCTCATGGGGCTCATGGAGCAGCAGAAGCACATCAATGAG 3225
            ||||||||||||| ||||||||||| || ||||||||||| ||||||||| || ||||||| ||
Db      421 ATCACCGCCCTGGCAGACTACGCCATGCGGCTTATGGAGCAAATGAAACACATCAACGAA 480

Qy     3226 CACTCCTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCCAGGT 3285
            ||| || | |||  | |||||| || |||  | |||||||||||||||||| |||||||
Db      481 CACTCTTTCAACAACTTCCAGATGAAGATCGGGTTGAACATGGGTCCGGTTGTAGCAGGT 540

Qy     3286 GTCATCGGGGCTCGGAAGCCACAGTATGAACATCTGGGGGACACCAGTGAATGTCTCTAGT 3345
            ||||||||||| | |||  |||||||| || | ||||||||||||||||||||||||||
Db      541 GTCATTGGGGCCCGGAAGCCCACAGTATGACATCTGGGGAAACACGGTGAATGTTTCCAGC 600

Qy     3346 CGTATGGACAGCACGGGGCTCCCCGACCGGGAATCCAGGTGACCACCGGACCTGTACCAGGTT 3405
            ||| ||||||||| ||||| |||| ||||||||||| ||||||  ||||| |||||||||||
Db      601 CGTATGGACAGCACGGGGCTCCCCGACCGGGAATCACAGGTGACCACCGGACCATCTACCAGGTT 660

Qy     3406 CTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGGGGTGTCGGTATTGCCCAGCACGTTGCCATGGAGATGAAAGA 3465
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                     /tissue_type="embryo"
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                     /clone_lib="UI-R-FJ0"
                     /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
                     UI-R-FJ0 is a cDNA library containing the following
                     tissue(s): rat embryo. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CATCTCTACT. This library
                     was created for the University of Iowa Program for Rat
                     Gene Discovery and Mapping (Val Sheffield, Bento Soares
                     and Tom Casavant)"
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Db    181 GCAGCAGGAGCGGCGGCTGCTCGTGTCCGTATTGCCCAGCACGTTGCCCATGAGGATGAAAGA 240
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Qy   1068 AGACATCAACCAACAAAAAAGAAGAACATGATGTTCCACAAGATCTACAGAAGCATGA 1127
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGACATCAACCAACAAAAAAGAAGAACATGATGTTCCACAAGATCTACAGAAGCATGA 300

Qy   1128 CAATGTCAGCATCCTGTTTGCAGACATTGAGGGGCTTCACCAGCCTGGCATCCCAGTGCAC 1187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAATGTCAGCATCCTGTTTGCAGACATTGAGGGGCTTCACCAGCCTGGCATCCCAGTGCAC 360

Qy   1188 TGCGGAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGC 1247
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCGGAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGC 420

Qy   1248 GGAGAATCACTGCCTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCT 1307
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGAGAATCACTGCCTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGGCT 480

Qy   1308 GCCCGGAGGCCCCGGGCCGACCGGCCGACCATGCCCACTGTCTGTGTGGGAGATGGGGGTAGACATGATTGA 1367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCGGAGGCCCCGGGCCGACCGGCCGACCATGCCCACTGTCTGTGTGGGAGATGGGGGTAGACATGATTGA 540

Qy   1368 GGCCATCTCGTGGTACGTGAGGTGACAGTGTGAAATGTGAACATGCGCGTGGGGCATCCA 1427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGCCATCTCGTGGTACGTGAGGTGACAGTGTGAAATGTGAACATGCGCGTGGGGCATCCA 600

Qy   1428 CA-GCGGGCGGCCGTGCACTGCGGCGTCCTTGG--CTTGCCGAAATGGCAGTT 1475
          || |||||||||||||| ||| ||||||||||||  |  |||||||||||||||
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="FN0181"
                     /note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
                     ; Site 2: SmaI; A mini-library was made by cloning
                     products derived from ORESTES PCR (U.S. Letters Patent
                     application No. 196,716 - Ludwig Institute for Cancer
                     Research) profiles into  the pUC 18 vector. Reverse
                     transcription of tissue mRNA and cDNA amplification were
                     performed under low stringency conditions."
BASE COUNT      125 a    203 c    193 g    155 t
ORIGIN
```

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Query Match             17.1%;     Score 607.8;  DB 10;   Length 676;
Best Local Similarity   97.3%;     Pred. No. 4.9e-120;
Matches  618;  Conservative   0;  Mismatches  17;  Indels   0;  Gaps   0;

Qy   1585 GAGGTGGAGCCAGGCCGTGGTGGCGAGCGCAAGCGGTACCTCAAGGAGCAGCAGCATTGAG 1644
          || ||| |||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      2 GACCAGCAGGGGTGGCGTGGTGGCGAGCGCAAGCGGTACCTCAAGGAGCAGCAGCATTGAG 61

Qy   1645 ACTTTCCTCATCCTGGGCGCCAGCCAGAAACGAAAGAGAGGAAGGCCATGCTGCCCAAG 1704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 ACTTTCCTCATCCTGGGCGCCAGCCAGAAACGAAAGAGAGGAAGGCCATGCTGCCCAAG 121

Qy   1705 CTGCGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCGCGGCTGGGTTCCTGATCGT 1764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CTGCGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCGCGGCTGGGTTCCTGATCGT 181

Qy   1765 GCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCGGGCCTTCCGCCAGATGGGCATTGATGATGATTCCAGC 1824
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCGGGCCTTCCGCCAGATGGGCATTGATGATGATTCCAGC 241

Qy   1825 AAAGACAACCGGGGACCACCCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTG 1884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 AAAGACAACCGGGGACCACCCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTG 301

Qy   1885 AGCCGTGCCATGCATGCCCGCAGCATTGATCAGCTGCGGAAGGACGTGCGCGGCGGTTT 1944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 AGCCGTGCCATGCATGCCCGCAGCATTGATCAGCTGCGGAAGGACGTGCGCGGCGGTTT 361

Qy   1945 CTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAGTACTCCCGGAAGGTGGATCCCGC 2004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 CTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAGTACTCCCGGAAGGTGGATCCCCGC 421

Qy   2005 TTCGGAGCCTACGTTGCCTGTGCCCGTTGGTCTTCTGCTTCATCCGCTTCATCCAGCTT 2064
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 TTCGGAGCCTACGTTGCCTGTGCCCGTTGGTCTTCTGCTTCATCCGCTTCATCCAGCTT 481

Qy   2065 CTCATCTTCCCACACTCCCATGCATGCTGGGATCATCATGCCAGCATCTTCCTGCTGCTG 2124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 CTCATCTTCCCACACTCCCATGCATGCTGGGATCATCATGCCAGCATCTTCCTGCTGCTG 541

Qy   2125 CTAATCACCGTGCTAATCGTGTCGTGTACTCCTGTGGTTCTCGTTCCCTAAGGCCCTG 2184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CTAATCACCGTGCTAATCGTGTCGTGTACTCCTGTGGTTCTCGTTCCCTAAGGCCCTG 601

Qy   2185 CAACGTCTCTGTCCCCAGCATTGTCCGCTCACGGGC 2219
          ||||||||||||||||||||||||||||||||||||
Db    602 CAACGTCTCTGTGCCCAGCATTGTCCGCTCCGGGGGC 636
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Qy  1009 CAGCAGGAGCGGCTGCTTCGGTATTGCCCCAGCACGTGCCCATGGAGATGAAAGAA 1068
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAGCAGGAACGCGTGCTGCTATCGGTGTTGCCCCAGCACGTGCCCATGGAGATGAAAGAA 420

Qy  1069 GACATCAACACAAAAAAGAGACATGATGTTCCACAGATCTACATACACAGAAGCATGAC 1128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACATCAACACAAAAAAGAGAGACACATGATGTTCCATAGATCTACATCCAGAAGCATGAT 480

Qy  1129 AATGTCAGATCCTCGTTTGCAGACATTGAGGGGCTTCACCAGCTGGATCCCAGTGCACT 1188
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Db   481 AATGTCAGATCCTCGTTTGCGGACATTGAGGGGCTTCACCAGCCTGGCCTCCCAGTGCACT 540

Qy  1189 GCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCG 1248
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCACAGGAACTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCG 600

Qy  1249 GAGAATCACTGCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGCTG 1308
         ||||||||||| ||||||||||||| || ||||||||||||||||||||||||||||
Db   601 GAGAATCACTGTCTGAGGATCAAGATCTTAGGAGACTGTTACTACTGCGGTGTCAGGGCTG 660

Qy  1309 CCGGAGGCCCGGCCGCCACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAG 1368
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Db   661 CCCGGAGGCCCGGCAGATCACCGCCCACTGCTGTGTGGAGATGGGGTAGACATGATCGAA 720

Qy  1369 GCCATCTCGCTGGTACGTGAG 1389
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Db   721 G-CATCTCGCTGGTGCCTGAG 740
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RESULT 13
CB247656
CB247656
LOCUS   CB247656   711 bp   mRNA   linear   EST 12-FEB-2003
DEFINITION UI-M-FIO-cea-e-22-0-UI.r1 NIH_BMAP_FIO Mus musculus cDNA clone
            IMAGE: 6836831 5', mRNA sequence.
ACCESSION   CB247656
VERSION   CB247656.1 GI:28369300
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 711)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            The following repetitive elements were found in this cDNA
            sequence: 369-390, >GC_rich#Low_complexity (matched compliment)
            530-597, >TIGGER1#DNA/MER2_type
            Seq primer: pYX-5.
FEATURES   Location/Qualifiers
     source   1..711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6836831"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 12.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FIO"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;

REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  AUTHORS   1 (bases 1 to 740)
  TITLE   NIH-MGC http://mgc.nci.nih.gov/.
  JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES   Location/Qualifiers
     source   1..740
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="UI-M-FIO-cau-i-13-0-UI"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 12.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FIO"
                     /note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     BonaIdo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CAGCCACGAC. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT   157 a   218 c   201 g   164 t
ORIGIN
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Query Match    16.9%;   Score 601;  DB 13;  Length 740;
Best Local Similarity   89.1%;  Pred. No. 1.4e-118;
Matches  660;  Conservative    0;  Mismatches   80;  Indels    1;  Gaps    1;

Qy   649 GGCATCCTGGGCGGCGCAGTCGGGGGGGCCTCTCGCAGCAGACCCGCCCAGCCCCTCT 708
         ||||||| || |||| |||| ||||||||||||||||||||||||||||| ||||||||
Db     1 GGCATCCTAGCAGCCGTGCAAGTCGGGGGTGCCCTGGCAGCCAATCCACACAGCCCCTCG 60

Qy   709 GCGGGCCTCTGTGCCCGTGTTCTTTGTCTACATCGCCTACACGCTCTCCCCATCCGC 768
         |||||| ||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db    61 GCGGGCCTTTGTGCCCCGTGTTCTTCGTCTTCATCACCTACACCACTCTTCTTCCCATTCGC 120

Qy   769 ATGCCGGGCTGCCGTCCTCAGCGGCCTGGGCCTTCCCACCTTGCATTTGATCTTGGCCTGG 828
         ||| || ||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   121 ATGCCGACCGCAGTACTCAGCGGCCTCGGGCGGCCTGGGCCTTCTCTACTCTGCATTTTGATTTTGGCCTGG 180

Qy   829 CAACTTAACCGGTGGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTCGTCGTGTTC 888
         ||||| ||| || |||| ||| ||||||||||||||||||||||||||| ||||||||||
Db   181 CAGCTGCAACAGCAGCGACCCCTTCCTTTGGAAGCAGCTCCGGTGCTCAACGTGGTGCTCTTC 240

Qy   889 CTCTGCACCAACGTCATTGGCATCTGCACACACTATCCAGCAGAGAGTGTCTCAGCGCCAG 948
         ||||||||||||| |||| ||| || ||| || |||||||||||||||||||||||||||
Db   241 CTCTGCACCAACATGCCATCGGTGTCTGCACACACTACCCTGCTGAAGTGTCTCAGCGGCCAA 300

Qy   949 GCCTTTCAGGAGACCCGCGGTTACATCCAGGCGCCCGGCTCCACCTGCAGCATGAGAATCG 1008
         ||||||||||||||||||||||| |||| |||||||||||||||||||||||||||||||
Db   301 GCCTTTCAGGAGGAGACCCGAGGTTACATCCAGGCGCCGGCGCTGCACCTGCAGCATGAGAACCGT 360

DEFINITION    603307455F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343565 5',
              mRNA sequence.
ACCESSION     BI691747
VERSION       BI691747.1    GI:15654376
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 1225)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Jeffrey Green M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM1872  row: n  column: 14
              High quality sequence start: 2
              High quality sequence stop: 693.
FEATURES             Location/Qualifiers
     source          1..1225
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5343565"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      351 a    322 c    370 g    182 t
ORIGIN

Query Match          16.3%;   Score 578.4;  DB 12;  Length 1225;
Best Local Similarity  87.8%;  Pred. No. 1.1e-113;
Matches  699;  Conservative  0;  Mismatches  91;  Indels  6;  Gaps  6;

Qy  2715 TGCGCTGGCCGCTGTATCTGCATGTCAGCAGGTGGAGTCGACTGCCGCCTAGACTTCCT 2774
         ||||||| ||||||||||||||||||||||||||||||||||| |||||||||||||
Db     8 TCCGCTGGCACTGTATCTGCATGCACATGCAATCGACTGCGCCGCCTGGACTTCCT 67

Qy  2775 CTGAAACTACAGGCAACAGGGGAGAAGGAGGATGGAAGGAGAAGGAGCTACAGGCATCACAACCG 2834
         |||||||||||||||||||||||||| | |||||||||||||||||||||||
Db    68 GTGGAAGTTACAGGCAACAGCGGGAGCAAGAGGGAGAAGGAGCTACAGGCATCACAACCG 127

Qy  2835 GAGGCTGCTGCATAAACATTCTGCCCAAGAACGTGGCGGCCCCACTTCCTGCCGCCGGAGCG 2894
         |||||| ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   128 GAGGTTGCTGCATAACAATTCTTCCCAAGAACGTGGCGCCGCCCACTTCCTGCCGCCGGGAACG 187

Qy  2895 CCGCAATGATGAACTCTACTATCATCGTCGTGTGAGTGTGCGTGTTATG-TTTGCCTCCA 2953
         |||||||||||||| ||||||||||||||||||||||||||||||| |||||||
Db   188 CCGCAACGATGAGCTGTACTACCAGTCGTGAATGTCGTGGCTGCGTGGCTGTTTGCCTCCA 247

Qy  2954 TTGCCAACTTCTCTGAGTTCTATGTGGAGCTGAGGCAAACAATGAGGGTGTCGAGTGCC 3013
         ||||||||||||||| ||||||||||||||||||||||||||||||||| |||||
Db   248 TCGCCAATTTCTCGGAGTTCTACGTGGAGCTCGAGGCAAACAACGAGGGGCTGGAGTGCC 307

Qy  3014 TGCGGCTGCTCAACGAGATCATCCTGACTTTGATGAGATTATCAGGAGGACGGTTCC 3073
         ||||||||||| |||||||||||||||||||||| ||||||||||||||||||
Db   308 TGCGGCTGCTCAATGAGATCATCGAGAATTTGACGAGATCATCAGTGAGGAGAGATTCC 367

Qy  3074 GGCAGCTGGAAAGATCAAGACAGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACG 3133
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

BASE COUNT     159 a    188 c    222 g    140 t    2 others
ORIGIN

Query Match          16.4%;   Score 583.4;  DB 14;  Length 711;
Best Local Similarity  91.6%;  Pred. No. 8.7e-115;
Matches  651;  Conservative  0;  Mismatches  56;  Indels  4;  Gaps  3;

Qy  1150 GACATTGAGGGCTTCACCAGCCTGCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACC 1209
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Db     1 GACATTGAGGGCTTCACCAGCCTGCCTCCCAGTGCACTGCACAGGAACTGGTCATGACC 60

Qy  1210 CTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATC 1269
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Db    61 TTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGTCTGAGGATC 120

Qy  1270 AAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCCCCGGCCGACCAT 1329
         |||||||||||||||||||||||||||||||||||||||||||||| ||
Db   121 AAGATCTTAGGAGACTGTTACTACTGCGTGTCAGGGTCAGGGGCCCCGAGGCCCGGGCAGATCAC 180

Qy  1330 GCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAG 1389
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTGCGTGAG 240

Qy  1390 GTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGGCCGGTGCACTGCCGGC 1449
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Db   241 GTAACAGGTGTGAACGTGAACATGCGCGTGGGCATCCACAGCGGACGTGTGCATTGCGGC 300

Qy  1450 GTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTGCCAAC 1509
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Db   301 GTCCTTGGCCTGCCTACGGAAATGGCAGTTTGATGTCTGGTCAAACGATGTGACCCTGCCTAAC 360

Qy  1510 CACATGGAGGCAGGAGGCCCGGGCTGGCCGCTGGCCGATCCAATCCACATCACTCGGGCAACACTGCAGTAC 1569
         |||||||||||||||| ||||||||||||||||| |||||||||||||||||||
Db   361 CACATGGAGGCCGGGGCCCGGGGCCGGGCCGCGGCCACATCACTCGGGCTACACTGCAGTAC 420

Qy  1570 CTGAACGGGGACTACGAG-GTGGAGCCAGGCCGTGGTGGCGAGCGCAACGCGTACCTCAA 1628
         ||||||||||||||||| | ||||||| ||||||||||||||||||||||||
Db   421 TTGAACGGGGACTATGAGNGTGGAGCCAGGCCGTGGTGTGAACCCAATGCGTACCTCAA 480

Qy  1629 GGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCAGAAACGGAAAAGAGGAGAA 1688
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Db   481 GGAGCAGTGCATTGAGACCTTCCTCATACTTGGGCCGCCAGCCAGAAACGGAAAAGAGGAGAA 540

Qy  1689 GGCCATGCTGGCCAAGCTGCAGCGGACTCGGGCGACTCCATGG-AAGGGCTGATGCCGC 1747
         |||||||||||||||||||||||| ||||||||||| ||||||
Db   541 AGCCATGCTGGCCAAGCTTCAGCGGACACGGGCGACTCCATGGNAAGGACTGATGCCCC 600

Qy  1748 GCTGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTTCCAAGGCCTTCCGCCAGATGG 1807
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Db   601 GCTGGGTTCCTGACCGTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCCGCCAGATGG 660

Qy  1808 GCAATTGATGATTCCAGCAAGACAACACGGGGCACCCAAGATGCCCTGAACC 1858
         |||||||||||||||||| ||| |||||| ||||||||||
Db   661 GCAATTGATGATTCTAGCAAGACAAGACAAC--GGGGTGCCAAGATGTCTGAACC 709

RESULT 14
BI691747
LOCUS       BI691747        1225 bp    mRNA    linear    EST 18-SEP-2001

BASE COUNT     278 a     295 c     312 g     158 t
ORIGIN

Query Match                16.1%;   Score 570.6;  DB 10;  Length 1043;
Best Local Similarity      87.6%;   Pred. No. 5.3e-112;
Matches  647;  Conservative  0;  Mismatches  89;  Indels  3;  Gaps  2;

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Qy  2774 TCTGAAACTACAGGCAACAAGAGGGAGAAGGAGGAGGAGGAGGAGCTACAGGCATACAACC 2833
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Db    10 TGTGGTGCCCACAGCAACAGGGAGCAGGGAGAAGGAGGAGGAGGAGGAGCTACAGGCATACAACC 69

Qy  2834 GGAGGCTGCTGCATAACATTCTGCCCAAGGACGTCGTGTGAGTGTGTGGCTGTTGTTTGCCTCCGGAGC 2893
         |||||  ||||||||||||||| |||||||||||||||   |  || |  ||| ||||| ||||   |||
Db    70 GGAGGTTGCTGCATAACATTCTTCCCAAGGACGTCGTGGCCGGCCGCCACTTCCTGCCCGGGAAC 129

Qy  2894 GCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGGCTGTTATGTTTGCCTCCA 2953
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Db   130 GCCGCAACGATGAGCTGTACTACCAGTCGTGTGAGTGTCATGTTGTGTCATGTTTGCCTCCA 189

Qy  2954 TTGCCAACTTCTCTGAGTTCTATGTGGAGTCGGAGCAAACAATGAGGGGTGTCGAGTGCC 3013
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Db   190 TCGCCCAATTTCTCGGAGTTCTACGTGGAGTCGGAGTCGGAGCAAACAACGAGGGGGTGCC 249

Qy  3014 TGCGCGTGCTCAACGAGATCATCGCTGCTTGATGAGATTATCAGCAGGAGCGGTTCC 3073
         ||||| ||| ||| |||||||||||| |  ||||||||| ||||| ||||| | ||||
Db   250 TGCGGCTGTCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGTGAGGAGAGATTCC 309

Qy  3074 GGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACACATGGCTGCTCAGGGCTGAACG 3133
         |||| |||||  |||||||||| | ||||||||||  ||||||||  || || | |  |
Db   310 GGCGGCTGGAGAAGATCAAGAACATCGGTAGCACCATCACATGGCCGCTCTGGCTGGCTGACTATGCCATGC 369

Qy  3134 CCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTCGCCCGCTGGCTACGCCATGC 3193
         ||||||||||  | |||||||||||||| ||||||||  |  |||||||||| |||||||
Db   370 CCAGCACCTATGACCAGGTCGGCCGCTCACACATCACGCGGCTGGCTATGCCATGC 429

Qy  3194 GGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCAGATGAAGA 3253
         |||||||||||||||||||  ||||||||||| ||||| ||||||||||||||||||||
Db   430 GGCTCATGGAGCAGATGAAACACATCAATGAACACTCTTTCAACAATTTCAGATGAAGA 489

Qy  3254 TTGGGCTGAACATGGGCCCAGTCGTGGCAGGTCATCGGGCTCGGAAGCCACAGTATG 3313
         | |||  ||||||||| ||  | ||  ||||  ||||||| | |||||||||||||||
Db   490 TCGGGTTGAACATGGGTCCGGTTGTAGCAGGCGTCATCGGGCCCGAAAGCCACAGTATG 549

Qy  3314 ACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGCGGGGTCCCCGACC 3373
         ||||||||||| |||| ||||||||| | |||||||||||||| || | |   |  ||||||
Db   550 ACATCTGGGGGAAATACCGTGAATGTCTCCAGTCGTATGGACAGCACTGGAGTGTCCTGACC 609

Qy  3374 GAATCCAGGTGACCACGGACCTGACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGT 3433
         |||| |||||||| ||||| |||||||||||||||||||||| ||||||||||||||||
Db   610 GAATACAGGTGACTACGGAGCTACAGGGACTATACCAGGTTCTAGCTGCCAAAGGCTACCAGCTGGAGG 669

Qy  3434 G-TCGAGGGGTGGTCAAGGTGAAGGGGCAAGGGGGAGATGAAGGGGGACCACCTACTTCCTCAATGGG 3492
         | | |||||||||||||||||||||| ||| ||| | ||||   | ||| |   ||| | ||| |||||
Db   670 GCCCGAGGGGTGGTCAAGGTGAAGGGGACAGGGGAGGACGGGGAAGATGAC--ACATACATCTCAAGGGGG 727

Qy  3493 GGGCCCCAGCAGTTAACAGG 3511
         |||| |||||||| || |||
Db   728 GGCACCAGCAGTAGCAAG 746
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VERSION   BG297229.1 GI:13060672
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SOURCE   Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1043)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10382 row: i column: 10
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                     Note: this is a NIH_MGC Library."

Search completed: January 7, 2004, 07:37:47
Job time : 7028 secs

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           GenCore version 5.1.6

           Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    January 7, 2004, 05:41:19 ; Search time 1421 Seconds
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Scoring table: IDENTITY_NUC
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Total number of hits satisfying chosen parameters:    4552328

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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3	3484.8	98.1	3549	10	US-09-750-240-5	Sequence 5, Appli
4	3443.2	96.9	3582	10	US-09-750-240-12	Sequence 12, Appl
5	1763.4	49.6	1812	10	US-09-750-240-3	Sequence 3, Appli
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7	883.4	24.9	2554	12	US-10-104-047-1856	Sequence 1856, Ap
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18	292.4	8.2	1180	10	US-09-915-582-11	Sequence 11, Appl
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ALIGNMENTS

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; Patent No. US2002010314741
; GENERAL INFORMATION:
;   APPLICANT: Hammon, H. K.
;   APPLICANT: Insel, P. A.
;   APPLICANT: Ping, P.
;   APPLICANT: Post, S. R.
;   APPLICANT: Gao, M.
;   TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
;   TITLE OF INVENTION: FAILURE
;   FILE REFERENCE: 22000205723
;   CURRENT APPLICATION NUMBER: US/09/750,240
;   CURRENT FILING DATE: 2001-10-12
;   PRIOR APPLICATION NUMBER: US 09/472,667
;   PRIOR FILING DATE: 1999-12-27
;   PRIOR APPLICATION NUMBER: US 08/708,661
;   PRIOR FILING DATE: 1996-09-05
;   NUMBER OF SEQ ID NOS: 13
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; SEQ ID NO 10
;   LENGTH: 3552
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;   PRIOR APPLICATION NUMBER: US 08/924,757
;   PRIOR FILING DATE: 1997-09-05
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Qy   2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGCC 2520

Qy   2521 ATGATCTTTGTCTTGGGGCTCATCTATTTTGGTGCTGCTTCGCTGGTCTCCCCCAGCCACC 2580
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Db   2521 ATGATCTTTGTCTTGGGGCTCATCTATTTTGGTGCTGCTTCGCTGGTCTCCCCCAGCCACC 2580

Qy   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTCCATTGCAATGAGACC 2640
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Db   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTCCATTGCAATGAGACC 2640

Qy   2641 TTTGATGGCTGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG 2700
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Db   2641 TTTGATGGCTGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG 2700

Qy   2701 ATTCTGCTGGTGTTTGCGCTGGCTCGTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC 2760
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Db   2701 ATTCTGCTGGTGTTTGCGCTGGCTCGTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC 2760

Qy   2761 CGCCTAGACTTCCTCTGAAACTACAGGCAACAGGGGAGGAAGGAGGATGGAGGAGCTA 2820
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Db   2761 CGCCTAGACTTCCTCTGAAACTACAGGCAACAGGGGAGGAAGGAGGATGGAGGAGCTA 2820

Qy   2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGCGCCCACTTC 2880
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Db   2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGCGCCCACTTC 2880

Qy   2881 CTGGCCCCGGAGCGCCGCCAATGATGAGCTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2940
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Db   2881 CTGGCCCCGGAGCGCCGCCAATGATGAGCTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2940

Qy   2941 ATGTTTGCCTCATTGCCAACTTCTCTTGAGTTCTATGTGGAGCTGGAGCAAACAATGAG 3000
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Db   2941 ATGTTTGCCTCATTGCCAACTTCTCTTGAGTTCTATGTGGAGCTGGAGCAAACAATGAG 3000

Qy   3001 GGTGTCAGTGCTGCTGCGCGCTGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
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Db   3001 GGTGTCAGTGCTGCTGCGCGCTGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060

Qy   3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGAATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGAATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120

Qy   3121 TCAGGGCTGAACGCACCTACGATCAGGTGGGCCGCTCCCACACTACTGCCCTGGCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TCAGGGCTGAACGCACCTACGATCAGGTGGGCCGCTCCCACACTACTGCCCTGGCT 3180

Qy   3181 GACTACGCCATGCGGCTCATGGAGCAGCAGATGAGCAATCAATGAGCACTCCTTCAACAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GACTACGCCATGCGGCTCATGGAGCAGCAGATGAGCAATCAATGAGCACTCCTTCAACAAT 3240

Qy   3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGTCATCGGGGTCGG 3300
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Db   3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGTCATCGGGGTCGG 3300
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Qy   3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTCTAGTCGTATGGACAGCACG 3360
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Db   3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTCTAGTCGTATGGACAGCACG 3360

Qy   3361 GGGGTCCCGACCAGTCAGGTGACCACGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
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Db   3361 GGGGTCCCGACCAGTCAGGTGACCACGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420

Qy   3421 TACCAGCTGGAGTGTGAGGGTTGGTCAAGGTGAAGGGGAGATGACCACCTAC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TACCAGCTGGAGTGTGAGGGTGTCGAGGGGTGGTCAAGGTGAAGGGGAGATGACCACCTAC 3480

Qy   3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540
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Db   3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540

Qy   3541 AAGGTGGGCACT 3552
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Db   3541 AAGGTGGGCACT 3552
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RESULT 2
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 99.8%; Score 3545.6; DB 14; Length 4942;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3548; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

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Qy      1 ATGTCATGGTTTAGTGGCGTTCCTGGTGTCCCTAAAGTGATGAACGAAAACAGCCTGGGGT 60
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Db    145 ATGTCATGGTTTAGTGGCGTTCCTGGTGTCCCTAAAGTGATGAACGAAAACAGCCTGGGGT 204

Qy     61 GAACGCAATGGGCAGAGCGGTTCGGCGGCCGCTCCGGCGCCGTCCGGCGGTCCACG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 GAACGCAATGGGCAGAGCGGTTCGGCGGCCGTTCCGGCGCCGTCCGGCGGTTCTCACG 264

Qy    121 CCCCGGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCAGGGCCCCC 180
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Db    265 CCCCGGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCACCCGCGGGCCCCC 324

Qy    181 CCTTCGGTGCCCCTGCCGCAGGATGACGGCCTTCATCCGGAGGGGGGGG 240
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Db    325 CCTTCGGTGCCCCTGCCGCAGGATGACGCCTTCATCCGGAGGGGGGGGG 384

Qy    241 GAGCTGGGGCGTCGCGGCAGTGGGCTCGGGCCTTCGAGGATACCGAGGTGACAACGACAGCG 300
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Db        GCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCGGCCATCTCGCTG  1524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381  GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGGTGGCATCCACAGCGGGCGCGTG    1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1525  GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGGTGGCATCCACAGCGGGCGCGTG    1584

Qy  1441  CACTCGGCGGTCCTTGCTTGCGGAAATGGCAGTTCGATGTGTGTTCAATGATGTGACC    1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1585  CACTCGGCGGTCCTTGCTTGCGGAAATGGCAGTTCGATGTGTGTTCAATGATGTGACC    1644

Qy  1501  CTGGCCAACCACATGAGGAGGAGGCCGGGCATCCGCCGCATCCACATCACTCGGGCAACA  1560
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Db  1645  CTGGCCAACCACATGAGGAGGAGGCCGGGCATCCGCCGCATCCACATCACTCGGGCAACA  1704

Qy  1561  CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCGGCCAGGCCGGTGGTGGCGAGCGCG   1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1705  CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCGGCCAGGCCGGTGGTGGCGAGCGCG   1764

Qy  1621  TACCTCAAGGAGCAGCACATTGAGACTTCCATGGGGCCGCCAGCCCAGAAACGGAAA     1680
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Db  1765  TACCTCAAGGAGCAGCACATTGAGACTTCCATGGGGCCGCCAGCCCAGAAACGGAAA     1824

Qy  1681  GAGGAGAAGGCCATGCTGGCCAAGTGCAGCCGACTCGGCGGCCAACTCCATGGAAGGGCTG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1825  GAGGAGAAGGCCATGCTGGCCAAGTGCAGCCGACTCGGCGGCCAACTCCATGGAAGGGCTG  1884

Qy  1741  ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGACCAAGGACTCCAAGGCCTTCCGC   1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1885  ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGACCAAGGACTCCAAGGCCTTCCGC   1944

Qy  1801  CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCCAGAGTGCCCGAACCCT     1860
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Db  1945  CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGGCACCCAGAGTGCCCGAACCCT     2004

Qy  1861  GAGGATGAGGTGGGATGAGTTCCATGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG  1920
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Db  2005  GAGGATGAGGTGGGATGAGTTCCATGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTG  2064

Qy  1921  CGGAAGGACCAATGTGCGCGCCGGTTTCTGCACCTTCCAGAGAGAGGATCTTGAGAAGAAG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2065  CGGAAGGACCAATGTGCGCGCCGGTTTCTGCACCTTCCAGAGAGAGGATCTTGAGAAGAAG  2124

Qy  1981  TACTCCCGGAAGGTGATCCCCGCTTCGGAGCTAGGTTGCCTGTGCCTGTTGGTCTTC    2040
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Db  2125  TACTCCCGGAAGGTGATCCCCGCTTCGGAGCTAGGTTGCCTGTGCCTGTTGGTCTTC    2184

Qy  2041  TGCTTCATCTGCTTCATCCAGCTTCCATCTTCCACACTCCACCCTGATGCTTGGGATC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2185  TGCTTCATCTGCTTCATCCAGCTTCCATCTTCCACACTCCACCCTGATGCTTGGGATC  2244

Qy  2101  TATGCCAGCATCTTCCTGCTGCTAATCACGGTGTGTGCTCCTGTGTGCTGTACTCCTGT  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2245  TATGCCAGCATCTTCCTGCTGCTAATCACGGTGTGTGCTCCTGTGTGCTGTACTCCTGT  2304

Qy  2161  GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2305  GGTTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCA  2364

Qy  2221  CATAGCACCCGCAGTTGGCATCTTTTCCGTCGCTTGTGTTTACTTCTGCCAAC       2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2365  CATAGCACCCGCAGTTGGCATCTTTTCCGTCGCTTGTGTTTACTTCTGCCAAC       2424

Qy  2281  ATGTTCACCTGTAACCAGTCAACCACACCCCATACGGAGCGCTGCAGCTGAATTTAACA  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2425  ATGTTCACCTGTAACCAGTCAACCACACCCCATACGGAGCGCTGCAGCTGAATTTAACA  2484

Qy  2341  CCTGCTGACATCACTGCCTGCACCTGCTCAATTACTCTCTGGGGCTCACGGGCA       2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2485  CCTGCTGACATCACTGCCTGCACCTGCTCAATTACTCTCTGGGGCTGGATGCT       2544

Qy  2401  CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2545  CCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG  2604
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Db        GAGCTGGGGGCTGCGGGCAGTGGCCCTGGCTTCGGAGGATACCGAGGTGACAACGACAGCG  444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301  GGCGGGACGGCTGAGGTGGCGCCCGACGCGCTGCCCAGGAGTGGGCGATCCTGCTGGCGC   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445  GGCGGGACGGCTGAGGTGGCGCCCGACGCGCTGCCCAGGAGTGGGCGATCCTGCTGGCGC   504

Qy   361  CGTCTGGTGCAGGTGTTCCAGTGGAAGCAGTTCCGTTCGGCCAAGCGGCCTGTAC       420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505  CGTCTGGTGCAGGTGTTCCAGTGGAAGCAGTTCCGTTCGGCCAAGCTGGACCACCTGTAC  564

Qy   421  CAGCGGTACTTCTTCCAGATGAACAACCAGCAGCCAGCCTGCTGATGGGCGTGCTGGTG   480
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Db   565  CAGCGGTACTTCTTCCAGATGAACAACCAGCAGCCAGCCTGCTGATGGGCGTGCTGGTG   624

Qy   481  CTGCTCACAGCGGGTGCTGCTTTCCACGCGCCGACCACCCGCCCTCAGCCTGCCTAT     540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625  CTGCTCACAGCGGGTGCTGCTTTCCACGCGCCGACCACCCGCCCTCAGCCTGCCTAT     684

Qy   541  GTGGGACTGTTGGCCTGTGCGCCGCCGCCCTGTTCGTGGGGTCATGGGGTCGGCATCGGG  600
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Db   685  GTGGGACTGTTGGCCTGTGCGCCGCCGCCCTGTTCGTGGGGTCATGGGGTCGGCATCGGG  744

Qy   601  CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAGTTACGTGGTGCTCGGGCATCCTGGGCG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745  CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAGTTACGTGGTGCTCGGGCATCCTGGGCG  804

Qy   661  GCAGTGCAGGTCGGGGCGCTCTCGAGCAGCAGCCCGCCAGCCCCCTCGCGGGCCCTCTGG  720
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Db   805  GCAGTGCAGGTCGGGGCGCTCTCGAGCAGCAGCCCGCCAGCCCCCTCGCGGGCCCTCTGG  864

Qy   721  TGCCCTGTGTTCTTTGTCTACACATCGGCCTCCTCCCCATCCGCGATGCGGGGCTGCC    780
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Db   865  TGCCCTGTGTTCTTTGTCTACACATCGGCCTCCTCCCCATCCGCGATGCGGGGCTGCC    924

Qy   781  GTCCTCAGCGCCTGGGCCTCCACTTGATCTTGGCCGCAACTTAACCGT          840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   925  GTCCTCAGCGCCTGGGCCTCCACTTGATCTTGGCCGCAACTTAACCGT          984

Qy   841  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTTGCCAATGTGCTCCTCTGCACCAAC     900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTTGCCAATGTGCTCCTCTGCACCAAC     1044

Qy   901  GTCATTGGCATCTGCACACACTATCCAGCAGCAGAGGTGTCTCAGCAGAGGCCTTTCAGGAG  960
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Db  1045  GTCATTGGCATCTGCACACACTATCCAGCAGCAGAGGTGTCTCAGCAGAGGCCTTTCAGGAG  1104

Qy   961  ACCCGCGGTTACATCCAGGGCCGGCTTCCACCAGCGCTCCAGCAGCATGGAGAATCGGCAGGAGCGG  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105  ACCCGCGGTTACATCCAGGGCCGGCTTCCACCAGCGCTCCAGCAGCATGGAGAATCGGCAGGAGCGG  1164

Qy  1021  CTGCTGCGTGTGCGGTTGCCCAGACGTTGCCATGGAGGATGAAAAGACATCAACACA    1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165  CTGCTGCGTGTGCGGTTGCCCAGACGTTGCCATGGAGGATGAAAAGACATCAACACA    1224

Qy  1081  AAAAAAGAAGACAGACATGATGTTCCACAAGATGTTCACAAGATCTACATACAGAAGCATGTCAGCATC  1140
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Db  1225  AAAAAAGAAGACAGACATGATGTTCCACAAGATGTTCACAAGATCTACATACAGAAGCATGTCAGCATC  1284

Qy  1141  CTGTTTGCAGACACCCTGGGGATGCTTGAGGGCTTCACCGAGGCGCGCAGGAGCTG    1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285  CTGTTTGCAGACACCCTGGGGATGCTTGAGGGCTTCACCGAGGCGCGCAGGAGCTG    1344

Qy  1201  GTCATGAGCCTTCCTCTGGATATTGCCCCAGGACGTTGACAAGGCTGGCTGCGAAGATCAGTCACTGC  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345  GTCATGAGCCTTCCTCTGGATATTGCCCCAGGACGTTGACAAGGCTGGCTGCGAAGATCAGTCACTGC  1404

Qy  1261  CTGAGGATCAAGATCTGGGGACTGTTACTACTGTGTCAGGGGTCTCAGGGCCCCGG   1320
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Db  1405  CTGAGGATCAAGATCTGGGGACTGTTACTACTGTGTCAGGGGTCTCAGGGCCCCGG   1464

Qy  1321  GCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCGGCCATCTCGCTG  1380
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Qy     2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
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Db     2605 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2664

Qy     2521 ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCACC 2580
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Db     2665 ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCACC 2724

Qy     2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
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Db     2725 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2784

Qy     2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2785 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG 2844

Qy     2701 ATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGCC 2760
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Qy     2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGGAGATGGAGGAGCTA 2820
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Db     2905 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGGAGATGGAGGAGCTA 2964

Qy     2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2965 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 3024

Qy     2881 CTGGCCCGGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 2940
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Db     3025 CTGGCCCGGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT 3084

Qy     2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3000
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Db     3085 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3144

Qy     3001 GGTGTCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
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Db     3145 GGTGTCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3204

Qy     3061 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
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Db     3205 GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3264

Qy     3121 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3265 TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3324

Qy     3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
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Db     3325 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3384

Qy     3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG 3300
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Db     3385 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGCTCGG 3444

Qy     3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3445 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3504

Qy     3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3505 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3564

Qy     3421 TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3565 TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3624

Qy     3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3625 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3684

Qy     3541 AAGGTGGGCACT 3552
            |||||||||| |
Db     3685 AAGGTGGGCATT 3696

RESULT 3
US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
;  APPLICANT: Hammon, H. K.
;  APPLICANT:  Insel, P. A.
;  APPLICANT:  Ping, P.
;  APPLICANT:  Post, S. R.
;  APPLICANT:  Gao, M.
;  TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
;  TITLE OF INVENTION:  FAILURE
;  FILE REFERENCE: 220002056723
;  CURRENT APPLICATION NUMBER: US/09/750,240
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 09/472,667
;  PRIOR FILING DATE: 1999-12-27
;  PRIOR APPLICATION NUMBER: US 09/008,097
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: US 08/924,757
;  PRIOR FILING DATE: 1997-09-05
;  PRIOR APPLICATION NUMBER: US 60/048,933
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: US 08/708,661
;  PRIOR FILING DATE: 1996-09-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 3549
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-750-240-5

  Query Match             98.1%;  Score 3484.8;  DB 10;  Length 3549;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 3517;  Conservative    0;  Mismatches   32;  Indels    3;  Gaps    1;

Qy        1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60

Qy       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120

Qy      121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180

Qy      181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240

Qy      241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300

Qy      301 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTGGCGC 360

Qy      361 CGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 420
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGTTTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC 420

Qy      421 CAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGCGGTGCTGGTG 480
            ||||||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Db      421 CAGCGGTACTTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 480
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Qy   1561 CTGCAGTACCTGAACGGGGACTACGAGGTGAGCAGCCAGGCCGTGGTGGCGAGCGCAACGCG 1620
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1558 CTGCAGTACCTGAACGGGGACTACGAGGTGAGCAGCCAGGCCGTGGTGGTGCAAGGCGCAAGCGCG 1617

Qy   1621 TACCTCAAGGAGCAGCACATTGAGACTTCCTCATCCTGGGCGCCAGCCAGAAACGAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1618 TACCTCAAGGAGCAGCACATTGAGACTTCCTCATCCTCGGGCGCCAGCCAGAAACGAAA 1677

Qy   1681 GAGGAGAAGGCCATGTGGCCAAGCTGCAGCGGACTCGGCCAACTCCATGAAGGGCTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1678 GAGGAGAAAGGCATGTGGCCAAGCTGCAGCGGACTCGGCCAACTCCATGAAGGGCTG 1737

Qy   1741 ATGCCGCGCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTCCAAGGCCTTCCGC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1738 ATGCCGCGATGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTCCAAGGCCTTCCGC 1797

Qy   1801 CAGATGGCATTGATGATTCAGCAAAGACAACCGGGCACCCAAGATGCCCTGAACCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1798 CAGATGGGCATTGATGATTCAGCAAAGACAACCGGGCACCCAAGTGCCCTGAACCCT 1857

Qy   1861 GAGGATGAGGTGGATGAGTTCCTGACGTGCCTGCAATCAGCAGCTG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1858 GAGGATGAGGTGGATGAGTTCCTGACGTGCCTGCAATCAGCAGCTG 1917

Qy   1921 CGGAAGGACCATGTGCGCCGGTTTCTGCTGCCAATGTGCTTCCAGAGAGAGGATCTTGAGAAGAAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1918 CGGAAGGACCATGTGCGCCGGTTTTTGCTCACTTCCAGAGAGAGGATTTTGAGAAGAAG 1977

Qy   1981 TACTCCCGGAAGGTGATCCCGCTTCGGAGCCTAGGTTGCCTGTGCCCTGTTGGTCTTC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1978 TACTCCCGGAAGGTGGATCCCGCTTCGGAGCGTACGTTGCCTGTGCCCTGTTGGTCTTC 2037

Qy   2041 TGCTTCATCTGCTTGCTGTGCTCCAGCTTCATCTTCCCACACTCCACCCTGATGCTTGGGATC 2100
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   2038 TGCTTCATCTGCTTGCTGTGCTCCAGCTTCTAATTTTCCCACACTCCACCCTGATGCTTGGGATT 2097

Qy   2101 TATGCCAGCATCTTCCTGCTGCTGGACACGTTGCCCATGGAGATGAAATAACACCGTGCTCCTGT 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2098 TATGCCAGCATCTTCCTGCTGCTGGACACGTTGCCCATGGAGATGAAATAACACCGTGCTCCTGT 2157

Qy   2161 GGTTCTCTGTTCCTAAGGCCCTGCAACGTCTGTCCCGCAACATTGTCCGCTCACGGGCA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2158 GGTTCTCTGTTCCTAAGGCCCTGCAACGTCTGTCCCGCAACATTGTCCGCTCACGGGCA 2217

Qy   2221 CATAGCACCCAGTTGGCATCTTTTCCGTCGTGTTTACTTCATCGGCACTTCATCGGAATC 2280
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   2218 CATAGCACCCAGTTGGCATCTTTTCCGTCGTGTTTACTTCGCTGGAATGTCCATTGCCAAC 2277

Qy   2281 ATGTTCACCTGTAACACACCCCATCAGCAGCTGTGCAGCAGAATCACTGC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2278 ATGTTCACCTGTAACACACCCCATCAGCAGCTGTGCAGCAGAGTTGGCC 2337

Qy   2341 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGATGCT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2338 CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGATGCT 2397

Qy   2401 CCCCTGTGTGAGGGACCAGTTGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAACATG 2460
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   2398 CCCCTGTGTGAGGGACCAGTTGGCACCATGCCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATG 2457

Qy   2461 CTGCTGAGGTCTTCTTGGCCAGTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2458 CTGCTGAGTCTTCTTGGCCAGTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517

Qy   2521 ATGATCTTTGTTCTTGGGGCTCATCTATTTGGTGCTGCTTCTTGGGGCCTGGATGCT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2518 ATGATCTTTGTTCTTGGGGCTCATCTATTTGGTGCTGCTTCTTGGGGCCTGGATGCT 2577

Qy   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTTCCATGGCGTTCTTCTTCCAATGAGACC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578 ATCTTTGACAACTATGACCTACTGCTTGGCGTTCCATGGCGTTCTTCTTCCAATGAGACC 2637

Qy   2641 TTTGATGGGGTGGACTGTCCAGCTGCGAGGGAGGGTGCCCTCAAATATATGACCCCGTGTG 2700
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Qy    481 CTGCTCTCACAGCCGGTGCTGCTGGCTTTCCACGCGCACCCGCCGCCCTCAGCCTGCCTAT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTGCTCTCACAGCCGGTGCTGCTGGCTTTCCAAGCCGCACCCGCCGCCCTCAGCCTGCCTAT 540

Qy    541 GTGGCACTGTTGGCCTGCCGCCGCCCTGTCGTGGGCGTCATGGTGGTGTGTAACCGG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGGCACTGTTGGCCTGCCGCCGCCCTGTCGTGGGCGTCATGGTGGTGTGTAACCGG 600

Qy    601 CATAGCTTCCGCCAGACTCCATGTGGGTGGTGAGTTACGTGGTGCTGGCATCCTGGGCG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTAACGTGGTGCTGGGCATCCTGGGCG 660

Qy    661 GCAGTGCAGGTCGGGGGCGCTTCTGCAGCAGACCCGCGCAGCCCTCTGCGGGCCTCTGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCAGTGCAGGTCGGGGGCGCTTTCGCAGCAGACCCGCGCAGCCCCTCTGCGGGGCCTCTGG 720

Qy    721 TGCCCTGTGTTCTTTGTACTATCGCCTACACGCCTACACGCTCCCCCATCCGCGGCGTGCC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGCCCTGTGTTCTTTGTATACATCGACATACACGCCTCCCCCATCCGCGGCGTGCC 780

Qy    781 GTCCTCAGCGGCCTGGGCCTTCCTCCAACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTCCTCAGCGGCCTGGGCCTTCCCAACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT 840

Qy    841 GGTGATGCCTTCCTCTGGAAGCAGCTTCGGTGCCAATGTGCTGTTCCTGCACCAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGTGATGCCTTCCTCTGGAAGCAGCTTCGGTGCCAATGTGCTGTTCCTGCACCAAC 900

Qy    901 GTCATTGGCATCTGCACACTATCTCAGCAGAGGTGTCTCAGCGCAGGCCTTTCAGGAG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAG 960

Qy    961 ACCCGCGGGTTACATCCAGGCCCGGCTTCACCTGCAGCATGAGAATCGGCAGCAGAGCGG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCCGCGGGTTACATCCAGGCCCGGCTTCACCTGCAGCATGAGAATCGGCAGCAGAGCGG 1020

Qy   1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGACATCAACACA 1080

Qy   1081 AAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1140
          |||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AAAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137

Qy   1141 CTGTTTGCAGACATTGAGGGGCTTCACCAGCCTGGCATCCGGGAGATCGGCGGCAGAGCTG 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 CTGTTTGCAGACATTGAGGGGCTTCACCAGCCTGGCATCCGGGAGATCGGCGGCAGAGCTG 1197

Qy   1201 GTCATGAGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 GTCATGAGGTGAGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1257

Qy   1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGGCTGCCGGAGGCCCGG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTGAGGATCAAGATCTTGGGGGGACTGTTACTACTGTGTGTCAGGGGCTGCCGGAGGCCCGG 1317

Qy   1321 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGGCCATCTCGCTG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGGCCATCTCGCTG 1377

Qy   1381 GTACGTGAGGTGACAGGTGTGAAATGTGAAACATGCCGCGTGGGCATCCACAGCGCGGCGTG 1440
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Db   1378 GTACGTGAGGTGACAGGTGTGAAATGTGAAACATGCCGCGTGGGCATCCACACGCGGGGCGTG 1437

Qy   1441 CACTGCGGCGTGCCTTGGCGGGACTCGGCCAGTTCGATGTGGTGTCCAATGATGTGACC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 CACTGCGGCGTGCCTTGGCGGGAAATGGCCAGTTCGATGTGGTGTCCAATGATGTGACC 1497

Qy   1501 CTGGCCAACCACCATGGAGGCAGAGGAGGCCCGGGCTGGCCATCCACATACTCGGGCAACA 1560
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Db   1498 CTGGCCAACCACCATGGAGGCAGAGGAGGCCCGGGCTGGCCATCCACATACTCGGGCAACA 1557
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Qy

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;  APPLICANT: Gao, M.
;  TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
;  TITLE OF INVENTION: FAILURE
;  FILE REFERENCE: 22000205672 3
;  CURRENT APPLICATION NUMBER: US/09/750,240
;  CURRENT FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: US 09/472,667
;  PRIOR FILING DATE: 1999-12-27
;  PRIOR APPLICATION NUMBER: US 09/008,097
;  PRIOR FILING DATE: 1998-01-16
;  PRIOR APPLICATION NUMBER: US 08/924,757
;  PRIOR FILING DATE: 1997-09-05
;  PRIOR APPLICATION NUMBER: US 60/048,933
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: US 08/708,661
;  PRIOR FILING DATE: 1996-09-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 12
;    LENGTH: 3582
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Modified AC-VI
US-09-750-240-12
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Query Match             96.9%;     Score 3443.2;   DB 10;  Length 3582;
Best Local Similarity   98.3%;     Pred. No. 0;
Matches 3491;  Conservative   0;  Mismatches   58;  Indels   3;  Gaps   1;
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Qy       1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT    60
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Db      22 AGGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT    81

Qy      61 GAACGCAATGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG   120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 GAACGCAATGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTCTCACG   141

Qy     121 CCCCGCTATATGAGCTGCCTCCGGATGACGAGAGCCACCCACCCCTGCGGGCCCC   180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 CCCCGCTATATGAGCTGCCTCCGGATGACGAGAGCCACCCACCCCTGCGGGCCCCC      201

Qy     181 CCTCCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGGCCAAG      240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     202 CCTCCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGGCAAGGCAAG   261

Qy     241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACAACGACAGCG   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     262 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACAACGACAGCG   321

Qy     301 GGCGGGACGGCTGAGGTGGCGCCGAGGAGTGGCGCGATCCTGCTGGCGC      360
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     322 GGCGGGACGGCTGAGGTGGCGCCGAGGAGTGGCGCGATCCTGCTGGCGC   381

Qy     361 CGTCTGGTGCAGGTGTTCCAGTGACGCAGTTCCGTCGGCGAGCGCCTGTAC   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     382 CGTCTGGTGCAGGTGTTCCAGTGACGCAGTTCCGTCGGCGAGCGCCTGTAC   441

Qy     421 CAGCCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGGGTGCTGGTG   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     442 CAGCCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGGGTGCTGGTG   501

Qy     481 CTGCTCACAGCGGTGCTGCTGGCTTCCACGCCGCCGCACCCGCCCTCAGCCTGCCTAT   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     502 CTGCTCACAGCGGTGCTGCTGGCTTCCACGCCGCCGCACCCGCCCTCAGCCTGCCTAT   561

Qy     541 GTGGCACTGTTGGCCTGTCGCGCCCGTTCGTGGGGCTCATGGTGGTGTGTAACCGG   600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     562 GTGGCACTGTTGGCCTGTCGCGCCCGTTCGTGGGGCTCATGGTGGTGTGTAACCGG   621

Qy     601 CATAGCTTCCGCCAGGACTTCCATGTGGTGGTAGTGTTGGTGCTCGGGCATCCTGGGCG   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     622 CATAGCTTCCGCCAGGACTTCCATGTGGTGGTAGTGTTGGTGCTCGGGCATCCTGGGCG   681
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Db    2638 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGAGGGTGGCCCTCAAATATATGACCCCTGGTG   2697
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Qy    2701 ATTCTGCTGGTGTTGCGCTGGCGCTGTATCTGCACTGCGATGCTCAGCAGGTGAGTGACTGCC   2760
           |||||||||||||||||||||||| |||||||||||||||
Db    2698 ATTCTGCTGGTGTTGCGCTGTGTTTGCGCTGCGCTGTATCTGCATTGCATGCTCAGCAGGTGAATCGACTGCC   2757

Qy    2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGGAGGAGGATGGGAGGAGCTA   2820
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    2758 CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGAGGAGGAGGATGGGAGGAGCTA   2817

Qy    2821 CAGGCATACAACCGGAGGGCTGCTGCGATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC   2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2818 CAGGCATACAACACAACCGGAGGGCTGCTGCGATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC   2877

Qy    2881 CTGGCCCCGGGAGCGGCGCCGCAATGATGAACTCTACATACAGTCGTGTGAGTGTGGCTGTT   2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2878 CTGGCCCCGGGAGCGGCGCCGCAATGATGAACTCTACATACAGTCGTGTGAGTGTGTGGCTGTT   2937

Qy    2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAAACAATGAG   3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2938 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAAACAATGAG   2997

Qy    3001 GGTGTCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC   3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2998 GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC   3057

Qy    3061 GAGGAGCCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACACATGGCTGCC   3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3058 GAGGAGCCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACACATGGCTGCC   3117

Qy    3121 TCAGGGCTGAACGCAGCCAGCACCTACGATCAGGTGGGCCCGCTCCCACATCACTGCCCCTGGCT   3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3118 TCAGGGCTGAACGCAGCCAGCACCTACGATCAGGTGGGCCCGCTCCCACATCACTGCCCCTGGCT   3177

Qy    3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT   3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3178 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT   3237

Qy    3241 TTTCAGATGAAGATTGGGCTGAACATGGCCCAGTCGTGCAGGTGTCATCGGGGTCCG   3300
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    3238 TTTCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGCAGGTGTCATCGGGGCTCGG   3297

Qy    3301 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG   3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3298 AAGCCACAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG   3357

Qy    3361 GGGGTCCCGACCGAATCCAGGTGACCACGGACCTGTAGCTGCCAAGGGC   3420
           ||||||||||||||||||||||||||||||||||||||| |||||||
Db    3358 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTAGCTGCCAAGGGC   3417

Qy    3421 TACCAGCTGGAGTGTCGAGGGGTCGTCAAGGTGAAGGGGAGATGACCACCTAC   3480
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    3418 TACCAGCTGGAGTGTCGAGGGGTCGTCAAGGTGAAGGGGGAGATGACCACCTAC   3477

Qy    3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC   3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3478 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC   3537

Qy    3541 AAGGTGGGCACT   3552
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Db    3538 AAGGTGGGCACT   3549
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```
RESULT 4
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US2002010314 7A1
; GENERAL INFORMATION:
;  APPLICANT: Hammon, H. K.
;  APPLICANT: Insel, P. A.
;  APPLICANT: Ping, P.
;  APPLICANT: Post, S. R.
```

This page contains a two-column nucleotide sequence alignment between query (Qy) and database (Db) sequences, with position numbers along each row.

Left column (positions 661–1758):

```
Qy   661  GCAGTCAGGTCGGGGCGGCTTCTCGCAGCAGACCCGCGGGGCCTCTGG  720
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   682  GCAGTGCAGGTGCGGGGCGGCTTCTCGCAGCAGACCCGCGGGGCCCTCTGG  741

Qy   721  TGCCCTGTGTTCTTTGTCTCACATCGGCTACACGGCTCCTCCCCATCGGCATGCGGCTGCC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   742  TGCCCGTGTGTTTCTTTGTCTCACATCGGCTACACGCGTCCTCCCCATCCGCATGCGGGCTGCC  801

Qy   781  GTCCTCAGCGGCCTGGGCGTTCTTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802  GTCCTCAGCGGCCTGGGCGTTCTTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGT  861

Qy   841  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCCAAC  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   862  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCCAAC  921

Qy   901  GTCATTGGCATCGCACACACTACTCAGCAGCAGAGGTGTCTCAGCAGGCCTTTCAGGAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   922  GTCATTGGCATCGCACACACTACTCAGCAGCAGAGGTGTCTCAGCAGGCCTTTCAGGAG  981

Qy   961  ACCCGCGGTTACATCCAGGCCCGGCTTCCACCTCCCAGCCAGGCCAGCGGCAGGAGGCGG  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   982  ACCCGCGGTTACATCCAGGCCCGGCTTCCACCTCCCAGCCAGGCCAGCGGCAGGAGGCGG  1041

Qy  1021  CTGCTGTCGTGTCGGTATTGCCCCCAGCACGTTGCCATGGAGATGAAAGAACATCAACACA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042  CTGCTGTCGTGTCGGTATTGCCCCCAGCACGTTGCCATGGAGATGAAAGAACATCAACACA  1101

Qy  1081  AAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGCAATGTCAGCATC  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102  AAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATGCAATGTCAGCATC  1161

Qy  1141  CTGTTTGCAGACATTGAGGGCTTCACCGGCTTCACCAGCCTGGCATCTTTCGCGCACTGCTG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1162  CTGTTTGCAGACATTGAGGGCTTCACCGGCTTCACCAGCCTGGCATCTTTCGCGCACTGCTG  1221

Qy  1201  GTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGC  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1222  GTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGGAGAATCACTGT  1281

Qy  1261  CTGAGGATCAAGATCTGGGGGACTGTTACTACTGGCCGGCCGTGTGTGTCAGGGCCCGGAGGGCCCGG  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1282  CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGGCCGGCCGTGTGTGTCAGGGCC---GGCCGGGC  1341

Qy  1321  GCCGACCATGCCCACTGCGTGTGTGGAGATGGGGGTAGACATGATTGAGGCGCATCTCGCTG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1342  GCAGATCACGCGCACTGCGTGTGTGGAGATGGGGGTAGACATGATTGAGGCGCCATCTCGCTG  1401

Qy  1381  GTACGTGAGGTGACAGTGTGAAATGTGAAATGCGCGGCGCATCCACAGCGGCGTG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1402  GTGCGTGAGGTAACAGTGTGAAACATGCGTGGGGCATCCACAGCGGCGACCGTG  1461

Qy  1441  CACTCGCGGCGTCCTTGGCCTTTGCGGGAAATGGCAGTTCGATGTGTGTCCAATGATGTGACC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1462  CATTCGCGGCGTCCTTGGCCTACGCAGGAAATGGCAGTTTGATGTGTCGTCAAACGATGTGACC  1521

Qy  1501  CTGGCCAACCAACCATGAGGCGAGGGCCGTGGCCGCATCCACATCACTCGGGCAACA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1522  CTGGCTAACCAACCATGAGGCGAGGGCCGGGGC---GGCCGGCGCGCCAACCATCACTCGGGCTACA  1578

Qy  1561  CTGCAGTACCTTGAACGGGGACTACAGAGGTGAGCCGCTGGTTGCGAGCGCAACGCG  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1579  CTGCAGTACTTGAACGGGGACTACAGAGGTGAGCCGCTGGTTGCGAGCGCAACGCG  1638

Qy  1621  TACCTCAAGGAGCAGCACCATTGAGACTTTCCTCATCCTCGGGGCGGGCCAGAAAACGGAAA  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1639  TACCTCAAGGAGCAGCAGTCATTGAGACCTTTCCTCATACTTGCGGGGCGGGCCAGAAAACGGAAA  1698

Qy  1681  GAGGAGAAGGCCATGCTGTCGGCCAAGCTGCAGCCGACTCGGGCGACTCCATGGGAAGGGCTG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1699  GAGGAGAAAGCCATGCTGTCGGCCAAGCTGCAGCCGACTCGGGCGACACGCGGCCAACTCCATGGGAAGGGACTG  1758
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Right column (positions 1741–2880):

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Qy  1741  ATGCCGGCTGGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCCTTCCGC  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1759  ATGCCCCGCTGGGTTCCTGACCGTGCCTTCTCCGGACCAAGGACTCTAAGGCATTCCGC  1818

Qy  1801  CAGATGGCATTGATGATTCCAGCAAAGACAACCGGGCACCGGGTGCCCAAGATGCCTGAACCCT  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1819  CAGATGGGCATTGATGATGATTCTAGCAAAGACAACACGGGCGGTGCCCAAGATGTCTGAACCCT  1878

Qy  1861  GAGGATGAGGTGGATGAGTTCCTGAGCCGGTGCCGTGCCGATGATGCCAGCAGCAGCATTGATCAGCTG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1879  GAAGATGAGGTGGATGAGTTCCTGGGCCGGTGCCGGGCCGATGCCAGCAGCAGCATTGATCAGCTG  1938

Qy  1921  CGGAAGGACCATGTGCGCGGCGGTTTCTGCTGCCTTCCAGAGAGGATCTTGAGAAGAAG  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1939  CGGAAGGACCATGTGCGCGGCGGTTTCTGCTGCCTTCCAGAGAGGATCTTGAGAAGAAG  1998

Qy  1981  TACTCCCGGAAGGTGGATCCCGCTTGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1999  TACTCCCGGAAGGTGGATCCCGCTTGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTC  2058

Qy  2041  TGCTTCATCTGCTTCATCCTGCTGCTCCAGCTTCTCATCTTCCCACACTTCCCACCCTGATGCGTGGGATC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2059  TGCTTCATCTGCTTCATCCTGCTGCTCCAGCTTCTCATCTTCCCACACTTCCCACCCTGATGCGTGGGATC  2118

Qy  2101  TATGCCAGCATCTTCCTGCTGCTCAATCACCGTGCGATCTGCTGTGCTGTGTGTGTACTCCTGT  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2119  TATGCCAGCATCTTCCTGCTGCTCAATCACCGTGCGATCTGCTGTGCTGTGTGTGTACTCCTGT  2178

Qy  2161  GGTTCCTGTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTTCCGCTTCACGGGCA  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2179  GGTTCTCTGTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTTCCGCTTCACGGGCA  2238

Qy  2221  CATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCCAGTGCCACCTGCCAATTACTCCTGGGCCTGGGATGCT  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2239  CATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCCAGTGCCACCTGCCAATTACTCCTGGGCCTGGGATGCT  2298

Qy  2281  ATGTTCACCTGTAACCACACCCCCATACGGAGCGTGTCAGCCCATAGGCTGAATTAACA  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2299  ATGTTCACCTGTAACCACACCCCCATACGGAGCGTGTCAGCCCATAGGCTGAATTAACA  2358

Qy  2341  CCTGCTGACATCACTGCCTGCCAGCGACTCGACGCTCAATTACTCTCTGGGCCTGGATGCT  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2359  CCTGCTGACATCACTGCCTGCCAGCGACTCGACGCTCAATTACTCTCTGGGCCTGGATGCT  2418

Qy  2401  CCCCTGTGTGAGGGCATCACATGCCCACCTGCCAGCTTCCTCGAGTACTTCATCGGGAACATG  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2419  CCCCTGTGTGAGGGCATCACATGCCCACCTGCCAGCTTCCTCGAGTACTTCATCGGGAACATG  2478

Qy  2461  CTGCTGAGGTCTCTTGGCCAGCTGCTCTGTCTTCCTGCACATCAGCAGCATCGGGGAAGTTGGCC  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2479  CTGCTGAGGTCTCTTGGCCAGCTGCTCTGTCTTCCTGCACATCAGCAGCATCGGGGAAGTTGGCC  2538

Qy  2521  ATGATCTTTGTCTTGGGCTCATCTATTTGGTGCTGCTCTGTCTGCGGGTTCCCCAGCCACC  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2539  ATGATCTTTGTCTTGGGCTCATCTATTTGGTGCTGCTCTGTCTGCGGGTTCCCCAGCCACC  2598

Qy  2581  ATCTTTGACAACTATGACCTACGCTTGGCGTCCAATGAGACC  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2599  ATCTTTGACAACTATGACCTACGCTTGGCGTCCAATGAGACC  2658

Qy  2641  TTTGATGGGCTGGACTGTCCAGCTGCCCTCAAAATATGACCCCCTG  2700
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Db  2659  TTTGATGGGCTGGACTGTCCAGCTGCCCCTCAAAATATGACCCCCTG  2718

Qy  2701  ATTCTGCTGGTGTTTGCGCTGCGCGTGTATCGTGCCTGCTCAGCCAGGTCGAGTCGACTGCC  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2719  ATTCTGCTGGTGTTTGCGCTGCGCGTGTATCGTGCCTGCTCAGCCAGGTCGAGTCGACTGCC  2778

Qy  2761  CGCCTAGGACATACAACCGGAGGCTGCTGGAAACTACAGAGGCAACAGGGGAGGAGGAGCTA  2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2779  CGCCTAGGACATTCCTCTGGAAACTACAGAGGCAACAGGGGAGGAGGAGGAGCTA  2838

Qy  2821  CAGGCATACAACCGGAGGCTGCTGCATAACATTCTCGCCCAGGACGTGGCGGCCCCACTTC  2880
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Db 2839 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2898

Qy 2881 CTGGCCCGGGAGGCCGCCAATGATGAACTTCTACTATCAGTCGTTGAGTGTGGCTGTT 2940
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2899 CTGGCCCGGGAGGCCGCCAATGATGAACTTCTACTATCAGTCGTTGAGTGTGGCTGTT 2958

Qy 2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2959 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3018

Qy 3001 GGTGTCGAGTGCGTCGCGGTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3019 GGTGTCGAGTGCGTCGCGGTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3078

Qy 3061 GAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACTTACATGGCTGCC 3120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3079 GAGGAGGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACTTACATGGCTGCC 3138

Qy 3121 TCAGGGCTGAACGCCAGCACCTACCAGCAGCCCGCTCCCACATCACTGCCCTGGCT 3180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3139 TCAGGGCTGAACGCCAGCACCTACCAGCAGCCCGCTCCCACATCACTGCCCTGGCT 3198

Qy 3181 GACTACGCGCCATGCCGGCTCATGGAGCAGAGAACATCAATGAGCACTCCTTCAACAAT 3240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3199 GACTACGCGCCATGCCGGCTCATGGAGCAGAGAACATCAATGAGCACTCCTTCAACAAT 3258

Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGCGTCATCGGGGCTCGG 3300
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3259 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGCGTCATCGGGGCTCGG 3318

Qy 3301 AAGCCACCAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3319 AAGCCACCAGTATGACATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3378

Qy 3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
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Db 3379 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3438

Qy 3421 TACCAGCTGGAGTGTCGAGGGCCCCAGCCAGTTAACAGGGGCCACAAATTCAGCTGAAGGGACC 3480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3439 TACCAGCTGGAGTGTCGAGGGGGTGGTCAAGGTGGTCAAGGGCAAGGGGAGATGACCACCTAC 3498

Qy 3481 TTCCTCAATGGGGGCCCCAGCCAGCAGTTAACACGGGGCCACAAATTCAGCTGAAGGGACC 3540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3499 TTCCTCAATGGGGGCCCCAGCCAGCAGTTAACACGGGGCCACAAATTCAGCTGAAGGGACC 3558

Qy 3541 AAGTGGGCACT 3552
        |||||||||||
Db 3559 AAGTGGGCACT 3570
```

RESULT 5
US-09-750-240-3

; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE

Query Match 49.6%; Score 1763.4; DB 10; Length 1812;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

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Qy 636 TTACGTGGTGCTGGCATCCTGGGCGGCAGTGCAGTCGGGGGCGCTCTCGCAGCAGACCC 695
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Db   3 TAACGTGGTGCTGGCATCCTGGGCGGCAGTGCAGTCGGGGGCGCTTTCGCAGCAGACCC 62

Qy 696 GCGCAGCCCCTCTGCGGGGCCTCTGTGCCCGTGTGTTCTTGTCATACATCGCCTACACGCT 755
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Db  63 GCGCAGCCCCTCTGCGGGGCCTCTGTGCCCGTGTGTTCTTTGTATACATCGCATACACGCT 122

Qy 756 CCTCCCCATCCGATCGCATGCGGGCGTGCGCTCTCAGCCGGCTGGCCTCTCCACCTTGCATTT 815
       |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 123 CCTCCCCATCCGATCGCATGCGGGCGTGCGCTCTCAGCCGGCTGGCCTCTCCACCTTGCATTT 182

Qy 816 GATCTTGGCCTGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGTCGGTGCCAA 875
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 183 GATCTTGGCCTGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGTCGGTGCCAA 242

Qy 876 TGTGTCGTGCTTCCTCTGCACCACACGTCATTGGCATCTGCACACAACTATCCAGCAGAGGT 935
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 243 TGTGTCGTGCTTCCTCTGCACCACACGTCATTGGCATCTGCACACAACTATCCAGCAGAGGT 302

Qy 936 GTCTCAGCGCCAGGCCTTTCAGGAGACCGGCTGCTGCTGCGGTATTGCCCCAGCAGTGCCAT 995
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Db 303 GTCTCAGCGCCAGGCCTTTCAGGAGACCGGCTGCTGCTGCGGTATTGCCCCAGCAGTGCCAT 362

Qy 996 GCATGAGAATCGGCACGGCAGGAGGCGGCCGACGTGTCGTGCTGCTGCTCGGT 1055
       |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 363 GCATGAGAATCGGCACGGCAGGAGGCGGCCGACGTGTCGTGCTGCTGCTCGGT 422

Qy 1056 GGAGATGAAAGAAGAAGACATCAACAACAAAAAAAAGAGAAGAC---ATGTTCCACAAGATCTACAT 1115
        |||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db  423 GGAGATGAAAGAAGAAGACATCAACAACAAAAAAAAGAGAAGACATCAACAACAAAAAAAAGAGAAGAC 479

Qy 1116 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 1175
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  480 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC 539

Qy 1176 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGTCTTTGCCCGGTTTGA 1235
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  540 ATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCTGAATGAGTCTTTGCCCGGTTTGA 599

Qy 1236 CAAGCTGGCTGCGCGGAGAATCACTGCCTGAGGATCAAGAGATCTTGGGGGACTGTTACTACTG 1295
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Db  600 CAAGCTGGCTGCGCGGAGAATCACTGCCTGAGGATCAAGAGATCTTGGGGGACTGTTACTACTG 659

Qy 1296 TGTGTCAGGGCTGCCGGAGGCCCGAGCCCACTGCGTGTGGAGATGGGGGT 1355
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 TGTGTCAGGGCTGCCGGAGGCCCGAGCCCACTGCGTGTGGAGATGGGGGT 719

Qy 1356 AGACATGATTGAGGCCATCTCGTTGGTACGTGAGGTGACAGGTGAATGTGAACATGCG 1415
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Db  720 AGACATGATTGAGGCCATCTCGTTGGTACGTGAGGTGACAGGTGAATGTGAACATGCG 779

Qy 1416 CGTGGGCATCCACAGCGGCGGCGTCGCACTGCGGCTCGTGTGGAGAATGCGCAGTT 1475
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Db  780 CGTGGGCATCCACAGCGGCGGCGTCGCACTGCGGCTCGTGTGGAGAATGCGCAGTT 839

Qy 1476 CGATGTGTGTCCAATGATGTGACCCTGGCCAACATGAGGCGAGGACCCGGGCTGG 1535
```

APPLICANT: Tomlinson, James
APPLICANT: Cor Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5027-01-US
CURRENT APPLICATION NUMBER: US/10/175,158
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13540
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 08/886,362
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
  LENGTH: 4523
  TYPE: DNA
  ORGANISM: human type V adenylyl cyclase
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (139)..(3921)
US-10-175-158-1

Query Match   49.6%;   Score 1761;   DB 15;   Length 4523;
Best Local Similarity 72.2%;   Pred. No. 0;
Matches 2385;   Conservative 0;   Mismatches 885;   Indels 33;   Gaps 6;

Qy   214 CGGAGGGGCGGCCCAGGCAAGGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGGCTTC 273
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Db   625 CGGGCGGCCAAGGGGCGCCGACGAGCTGGAGGCGCCGCCGCCTCGAGGCGGCGGCCGGGAG 684

Qy   274 GAGGATACCGAGGTGACAACGACAGCGGCGGGACCGGCTGAGGTGGCGCCCGACGCGGTG   333
          | ||| |||||| | | |||||| ||||||| |||||||||| ||| |||| |||
Db   685 GGGTCCGGGGATGGCCGCAGCTGGGCTCGGGCGCGTCGGGCGGCCCCGCGCGCGCGCGTG   744

Qy   334 CCCAGGAGTGGGCGGCGATCCTGCTGCCCGTCGGTGCGGCTGTTCCAGTCGAAGCAGTTC   393
          ||| ||||| ||||||||| | |||||||| |||||||| || |||||||
Db   745 C---TGTCCCGTGGGCGCCTGCTGGCGTTGCTGCAGATATTCCGCTCCAAGAAGTTC   801

Qy   394 CGTTCGGCCAAGCTGGAGCGCCGCCTGTACCAGCGGCGTACTCTTCTGCAGATGAACCAGAGCAGC   453
          ||||||||| ||||||| ||||| |||| |||||| ||| ||| |||||| ||||| ||||
Db   802 CCGTCGGACAAACTGGAGCGCGTGTACCAGCGGCGTACTTCTCCGCGCTGAACCAGAGCAGC   861

Qy   454 CTGACCGCTGCTGATGGCGGTGCTGCTCACAGCGGTGCTGCTCACAGCGGTGCTTTCCACGCC   513
          ||| | | || ||||| ||||||||| ||||| ||||| |||| ||||||||||
Db   862 CTCACCATGCTCATGGGCGTCGTGGTGTCTCGTGTGCCTCGGCGGCGCCCTTCCACGCG   921

Qy   514 GCACCCGCCCCCGCCCTCAGCCTGCCTCATGTGGCTGACCTGTTGGCGCGGTGCTGCTTGTTC   573
          ||||| ||| |||||| ||| ||||| ||| ||||| |||||| | ||||||||
Db   922 GCGCGGCGCCCCCGCTGCCCTCACCTGCCGCGTGCTGCGGCCGCCGCGTCGGCGTGATC   981

Qy   574 GTGGGGCTCATGTGTGTGTAACCGGACATAGCTTCCGCCAGGACTCCATGTGGGTGTG   633
          | |||||||| |||||| |||| ||||||||| |||||| |||| |||||||||||
Db   982 CTCATCATGGCTGTGCTTTGCAACCGCGCCGCCTTCACCAGGACCACCATGGGCCTGGCC   1041

Qy   634 AGTTACGTGGTGCTGGGCATCCTGGGCCAGTGCAGGTGCGGGGGCCGCTCTGCAGCAGAC   693
          | |||| ||||||| ||| ||||| |||| |||| ||| |||||| ||||||||
Db   1042 TGCTATGCGTCATCGCCGTGTGTCATCGTGCTGCTCCAGGTGGTGGGCCTGTGCCCGCAG   1101

Qy   694 CCGGCGCAGCCCCTCGGGGCCTCTCGGGGCCTCTCACACG   753
          || | || ||| ||||| || |||||| | ||||||||||||| ||||||||||||||| |||||||
Db   1102 CCACGGAGCGCGCCTCTGAGGGCCATCTGGTGGACCGGTGTTCTTCATCTTCACACTACACG   1161

Qy   754 CTCCTCCCATCCGCATGCGGGCTGCGTCCTCAGCCGCCTGCTCCGCCCCTCCAC   813
          ||| ||| | || | | || ||| | | | |||||| || ||| || |||
Db   1162 CTGCTGCCGGTCGCCGTGGCATGGCGCCGAGTGCTTCAGCGGGGTGCTCTCGGGG   1221

Qy   814 TTGATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCGGAAGCAGTTCGGTGCC   873
          || |||||| |||| || | || | | | || | |||||| ||||| |||||
Db   1222 CTGGCCATGCCCATGCCGGTCCATCCGCCACCAACCGCCCAGGACACCAGTTCCTGCTGAAGCAGTTCCTGTGTCTCC 1281

RESULT 6
US-10-175-158-1
; Sequence 1, Application US/10175158
; Publication No. US2003008371A1
; GENERAL INFORMATION:

Db   840 CGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGAAGCAGCAGGAGCCGGGCTGG   899
          ||||||||||||
Qy   1536 CCGCATCCACATCACTCGGCCAACACTGCAGTACCTGAACCGGGACTACGAGGTGGAGCC   1595
          ||| ||||||||
Db   900 CCGATCCACATCACTCCGGCCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCC   959

Qy   1596 AGGCCGTGGTGGCGAGCGCAACGCGTACCTCAAGGAGCAGCAGCATTGAGACTTTCCTCAT 1655
          |||| ||||||||||| ||||||||
Db   960 AGGCCGTGGTGGCGCAACGCAACGCGTACCTCAAGGAGCAGCAGCATTGAGACTTTCCTCAT 1019

Qy   1656 CCTGGGCGCCAGCAGAAACGGCAGAAGAGGAGAAGGCCATGCTGGCCAAGCTGCAGCGGAC 1715
          |||||||
Db   1020 CCTGGGCGCCAGCAGAAACGGCAGAAGAGGAGAAGGCCATGCTGGCCAAGCTGCAGCGGAC 1079

Qy   1716 TCGGGGCCAACTCCATGGAAGGGCTGATGCCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCG 1775
          ||||||
Db   1080 TCGGGGCCAACTCCATGGAAGGGCTGATGCCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCG 1139

Qy   1776 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGCCATTGATGATTCCAGCAAAGACAACCG 1835
          ||||||
Db   1140 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACACACCG 1199

Qy   1836 GGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGGTGAGTTCCTGAGCCGTGCCAT 1895
          ||||||
Db   1200 GGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGGTGAGTTCCTGAGCCGTGCCAT 1259

Qy   1896 CGATGCCGCAGCATTGATCAGCTGCGGAAGACCATGTGCGCCGGTTTCTGCTCACCTT 1955
          ||||||
Db   1260 CGATGCCGCAGCATTGATCAGCTGCGGAAGACCATGTGCGCCGGTTTTTGCTCACCTT 1319

Qy   1956 CCAGAGAGAGATCTTGAGAGAAGTACTCCCGGAGGTGGATCCCCGCTTCGGAGCCTA 2015
          ||||||
Db   1320 CCAGAGAGAGATTTTGAGAGAAGTACTCCCGGAGGTGGATCCCCGCTTCGGAGCCTA 1379

Qy   2016 CGTTGCCGTGTCCCTGTGTTCTTCGCTTCATCTGTCATCTGTTCTCATCTTCCC 2075
          ||||||
Db   1380 CGTTGCCGTGTCCCTGTGTTCTTCGCTTCATCTGTTCATCTGTTCTAATTTTCCC 1439

Qy   2076 ACACTCCACCTGATGCTTGGGATCTATGCCAGCATCTTCCTGCTGTCTGCTAATCACGGT 2135
          ||||||
Db   1440 ACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGTCTGCTAATCACCGT 1499

Qy   2136 GCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCGAACGTCTGTC 2195
          ||||||
Db   1500 GCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCGAACGTCTGTC 1559

Qy   2196 CCGGCAGCATTGCCGCTCACGGGCCACATAGCACACCGCAGTGCATCTTTTCCGTTCCTGCT 2255
          ||||||
Db   1560 CCGCAGCATTGTCCGCTCACGGGCCACATAGCACACCGCAGTGCATCTTTTCCGTTCCTGCT 1619

Qy   2256 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACACCCCATACGGAGACTG 2315
          ||||||
Db   1620 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACACCCCATACGGAGACTG 1679

Qy   2316 TGCAGCCCGACATGCTGAATTAACACACCTGCTGACATCACTGCCTCAGCAGCT 2375
          ||||||
Db   1680 TGCAGCCCGGATGCTGAATTAACACACCTGCTGACATCACTGCCTGCACCTGCAGCAGCT 1739

Qy   2376 CAATTACTTCTTCTCGGGCTCCGATGCTCCCCTGTGTGAGGCCGCACCATGCCCACCTGCGCTT 2435
          ||||||
Db   1740 CAATTACTTCTTCTCGGGCTCCGATGCTCCCCTGTGTGAGGGCGCACCATGCCCACCTGCGCTT 1799

Qy   2436 TCCTGAGTACTTC 2448
          ||||| ||
Db   1800 TCCTGAGGTGTTC 1812

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Db   3430 CGGCTACTCAATGAGATCATCGCTGACTTTGATGAGATCAACATCAGCGAGGATCGGTTCCGG 3489
          |||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy    294 CCTTCCCGTCATGTTGCCATGGAGATGAAAGCAGACATCAACGCCAGCCAAGCAGGAGGATAT  353

Qy   3076 CAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCC 3135
          |||||| |||| || ||  |||| || ||||||||||||||||||||| ||
Db   1095 GATGTTCCACAGATCTACATCAGAGGATGCATGAGAGCATGACAATGTCAGCATCTTGCAGACAT 1154

Db   3490 CAGCTCGAAGAGATCAAGAGATCAAGACCATCGGCACGACCTACGACCTGCTGCCTCCCGGCAC 3549
          |||||| ||||| |||||||||||| |||||||||||||||||||
Qy    354 GATGTTCCATAGATTTACATCCAGAAACATGACAACATGACAACATGCTCTGTTTGCTGACAT  413

Qy   3136 AGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCTGCTGACTACGCCATGCGG 3195
          || |||||||||||||||| |||||||||||||||||||||||||||
Db   1155 TGAGGGCTTCACCAGCTCCAGTGCACTGCGCAGTGGCTCGTCATGCAGGTCATGACCCTGAA 1214

Db   3550 TCTACCTACGACAAGGTGGGCAAGACCCACACTGCACTGGCCGCTTTGCCATGAAG 3609
          |||| || ||||||||||||||||||||||||||||| ||
Qy    414 CGAGGGGCTTCACCAGCTGCGGCTCCCAGTGGCGACTGCGACAGGAACTGGTCATGACCCTCAA  473

Qy   3196 CTCATGGAGCGATGAAGCACACATCAATGAGCACTCCTTCAACAATTCCAGATGAAGATT 3255
          ||| ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   1215 TGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATGAACTACTGCTGGAGGATCAAGAT 1274

Db   3610 CTGATGGACCAGATGAAGTAGCATCAATGAGCACTCCTTCAACAACTTCAGATGAAGATC 3669
          |||| ||||||||||||||||||| ||| || |||||||||| ||||||||||
Qy    474 CGAGCTCTTCGGCCCGCTTTGACAAGTGGCCGCAGAGAATCACTGTTTACGTATTAAGAT  533

Qy   3256 GGGCTGAACATGGCCCAGTCGTGGCAGGTGTCATCGGGCGTCGGAAGCCACAGTATGAC 3315
          |||||| ||||||||||||| || ||||||||||||||||||||||| ||
Db   1275 CTTGGGGACTGTTACTACTGTGTGTCATCGGGCGTCGGGGCTGCCGGGGGCCGACATGCCCA 1334

Db   3670 GGGCTCAACATCGGCCCCGTGTGGCGGGTGTGATAGGGGCACGAAAGCCTCAGTACGAC 3729
          |||||| |||| || || || || ||||||| |||| |||||||||| ||
Qy    534 CCTTGGGGATTGTTATTACTGCGTCTCGGGGTGTCGGGGCTGCCTGAAGCAAGGGCCGACCGCCCA  593

Qy   3316 ATCTGGGGAACACAGTGAATGTCTCTAGTCGTATGGACACAGCACGGGGGTCCCCGACCGA 3375
          ||||||||| || ||||||||||| || || ||||||||||| |||||| ||
Db   1335 CTGCTGTGTGAGATGGGGGTAGACATGATTGAGGGCATCTCGCTGTGTACTGAGGTGAC 1394

Db   3730 ATCTGGGGCAATACCGTGAACGTGGCCAGCTGGCCAGCAGCAGTAACCGTGTACCCGACCGC 3789
          |||||||| ||| ||||| || || ||||||||| ||||||| ||||||
Qy    594 CTGCTGTGTGGAGATGGCAGTGGCATGGGACATAGATCGAGGGCATCTCGTTCGGCGGAGGTGAC  653

Qy   3376 ATCCAGGTGACCACCGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGT 3435
          |||||||||||||||||||||| ||||||| |||| ||||||||||||||
Db   1395 AGGTGTGAATGTGAACATGCGCGTGGCGCATCCACAGCCGGTGCAACACTGCCGTCCT 1454

Db   3790 ATCCAGGTGACCACCACAGATACCAGGTGCTGGCTGCTGCCAACACGTGACCGTGGAGTGC 3849
          |||||||||||||| || ||||||||| || |||||||||| ||||||||
Qy    654 AGGGGTGAACGTGAACATGCGTGTGGGAATTCACAGCGGGGGCGAGTACACTGCGGTGTCCT  713

Qy   3436 CGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCCTCAATGGGGGC 3495
          ||||||| |||||||||||||||||| ||||||||||||||||||||
Db   1455 TGGCTTCGGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACAT 1514

Db   3850 CGGGGCCTGGTCGGTCAAGGTCAAGGGCAAAGGGCGAGATGATGAGGGCAAGGGGCAATGGGGGC 3909
          ||||||| |||||||||| ||| ||||||||||||||||||| |||||| ||
Qy    714 TGGTCTCCAGGAAGTGGCAGTTCGACGTCTGTGTCGGTCGTCTAACGAGTCAACTACCAACCACAT  773

Qy   3496 CCC 3498
          |||
Db   3910 CCC 3912

Qy   1515 GGAGGAGGAGCCGGGCTGGCCGCATCCACATCACTCGGGCAACACTGCAGTACTTGAA 1574
          |||||||| |||||||||||||||||||||||| ||||||||
Db    774 GGAGGCTGGCGGCAAGGCAGGCAGCGCATCCACATCACCACAAGGTCACACTACCTGAA  833

Qy   1575 CGGGGGACTACGAGGTGGAGCGTGGGGGCGAGCGCAACGGCCGTACCTCAAGGAGCA 1634
          ||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db    834 TGGGGGACTACGAGGTGGAGCGTGAGCGGCGCAACGCGCCTACCTCAAGGACCA  893

Qy   1635 GCACATTGAGACTTTCCTCATCCTCTGCGGTCGGGCGCAGCCCAGAAACGGAGGAGGCCAT 1694
          ||||||||||| |||||| |||||| ||||| || ||||||||||
Db    894 CAGTATCGAGACTTCCTCATCCTCTGCGTCACCCGAGCGGAAAGAGAAAGAGAAGGCCAT  953

Qy   1695 GCTGGCCAAGCTGCAGCGGACTCGGCGACTCCATGGAAGGGCTGATGCCGCGCTGGT 1754
          ||||||||||||||||| || ||||| |||||||||||||||||||||
Db    954 GATCGCCAAGATGAACTGCCAGAGAACCAACTGCCATCGGGCACAACCCACCACTGGG 1013

Qy   1755 TCCTGATCGTGCCTTCTCC--------------CGGACCAAGGACTCCAAGGGCTTCGCGCCA 1802
          |||||||||||| | |||||              ||||| |||||||||| ||
Db   1014 GGCTGAGCGCGCCCCTTCTACAACCACCTGGGTTGCAACCAGGTGTCCAAGGAGATGAAGCG 1073

Qy   1803 GATGGGCATTGATGATTCCAGCAAAGACAACGGGGCACCCAAGATGCCCAAGCCCTGA 1862
          |||||||| |||||| ||| | || ||||| |||||||||||||||
Db   1074 GATGGGCTTTGAAGACCCCA-----AGGACAAGAACGAACGCCCCAGGAGAGTGCGAACCCTGA 1127

Qy   1863 GGATGAGGTGGATGAGTTCCTGACGCCGTGCCATGATGCCCGCAGCATTGATCAGCTGCG 1922
          |||||||||||||||||||| ||| ||||||||||||| ||||
Db   1128 GGATGAAGTGGATGAGTTCCTGGTGCGCCAGGAGCATTGATAGGCTTCG 1187

Qy   1923 GAAGGACCATGCGGCGGTCGGTGGCCGGGTTCTCGTGTTCGCTGCACCAACGTCATTGGCATCTG 1982
          |||| ||||||| || || || ||||| ||||||||| |||||| ||| |||||||||
Db   1188 GTCTGAGCACGTCCGCAAGTTCCTCCTGACCTTCAGGGAGCTGACTTAGAGAAGAAGTA 1247

Qy   1983 CTCCCGGAAGTGGATCCCCGCTTCGAGGCCTTTCAGGAGCACCGGCGCGGTTACAT 2042
          ||| ||||||| || ||| || || || |||| || ||| |||| ||
Db   1248 CTCCAAGCAGTAGACGAGACCGATTTGGTGCCTTATGTGGCCTCGTCGCTCTTCCT 1307

Qy   2043 CTTCATCTGCTTCATCCTGCACTCCAGCTTCTCATCTTCCCACACTCCCACCTGATAGCTTGGGATCTA 2102
          |||||| |||| ||||| ||| || || |||| | ||
Db   1308 CTTCATCTGCTTTGTCCAGATCACCATCGTGCCCCACTCCATATTCATGTCTCAGCTTCTA 1367

Qy   2103 TGCCAGCAACATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTCGTGCGTCTCCTGTGG 2162
          | ||||||
Db   2103 TGCCAGCAACATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTCGTGCGTCTCCTGTGG
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RESULT 7
US-10-104-047-1856
; Sequence 1856, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1856
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1856

Query Match   24.9%;   Score 883.4;   DB 12;   Length 2554;
Best Local Similarity   71.8%;   Pred. No. 5.7e-241;
Matches 1208;   Conservative 0;   Mismatches 451;   Indels 24;   Gaps 3;

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Qy    855 CTGGAAGCAGCTCGGTGCCAATGTGCTCTGTTCCTCTGCACCAACGTCATTGGCATCTG 914
          ||||| |||||||||||| ||||| ||| | ||||||||||||||||||
Db    114 CAGTGAAGAAGCTTGTCGTCTCCAATGTTCTCCATTTTCTCCTGCACCATCGTGGGTGTCTG 173

Qy    915 CACACTACTATCCAGCAGAGAGGTGTCTCAGCGCGCCAGGCCTTTCAGGAGCGACCGCCGGGTTACAT 974
          |||| ||| |||||||| ||||||||||||||||||| |||
Db    174 CACCCACTATCCGGCTGCGAGGTGCCCCCAGAGACAGGCTTTCCAGGAGCCCGAGAGTGCAT 233

Qy    975 CCAGGCCCGCCGGCTCCACCTGCTGCTCGCAGCATGGAGAATCGGCACGAGAATGCAGCGGCGGCTGCTGTCGCGGT 1034
          |||||||| ||||||| |||| |||||||||||| ||
Db    234 CCAGGGCGCGGCTCCACTCGCAGTCGGAGCAGTCGGAGGAACCGGCAGGAACCGGCTCCTGCTTCCTTGCTTCTCTGT 293

Qy   1035 ATTGCCCCAGCACGTTGCCATGGAGATGGAGAATGAAAGAAGACATCAACACAAAAAAGAAGACAT 1094
          | ||||||
Db   2103 TGCCAGCAACATCTTCCTGCTGCTAATCACCGTGCTGATCGTGCTCGTGCGTCTCCTGTGG 2162
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Db   1368  CCTGACCTGTTCCCTGCTGCTGACCTTGGTGGTGTTTGTGTCTGTGATCTACTCCTGCGT  1427
                 ||||||  |||||    ||||||    ||||| |||     |||  |||||  ||
Qy   2163  TTCTCTGTTCCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACA  2222

Db   1428  AAAGCTCTTCCCCTCCCCACTGCAGACCCTCTCCAGGAAGATCGTGCCGGTCCAAGATGAA  1487
                |||||     |||||    |||||| ||||||  || ||||| ||||| ||||||
Qy   2223  TAGCACCGGAGTTGGCATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACAT  2282

Db   1488  CAGCACCCTGTTGGGGTGTTCACCATCACCCTGGTGTTCCTGCGGCTTTTGTCAACAT  1547
                |||||   |||||||   ||  ||||| |||   ||   |||  ||||||
Qy   2283  GTTCACCTGTAACCACACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAACACC  2342

Db   1548  GTTCACGTGCAACTCCAGGGACCTGCTGGGCTGCTTGGGCACAGAGACAACATCAGCGC  1607
                |||| ||    |  |||| ||   ||  |||||| ||  ||
Qy   2343  TGCTGACATCACTGCCTGCCACCTGCAGCAG------CTCAATTACTCTCTGGGCCTGGA  2396

Db   1608  GAGCCAGGTCAACGCGTGTCACGTGGCGGAGTCGGCCCGTCAACTACGGGCCTGGGCGATGA  1667
                ||||||  |  ||| || |||| |||| ||||||| ||||||
Qy   2397  TGCTCCCCGTGTGTGAGGGGCCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAA  2456

Db   1668  GCAGGGCTTCTGTGGCAGCCCCTGCCCCAACTGCAACTTCCCCGAGTACTTCACCTACAG  1727
                  ||| |  ||||||  ||||||  |  |||| ||||||||||||   |||
Qy   2457  CATGCTGCTGAGTCTTCTTGGCCAGCTCTGTCTTCTCCTGCACATCAGCAGCATCGGGAAGTT  2516

Db   1728  CGTGCTGCTCAGCCTGGCCTGGCCTCGGCCTCCGTGTTCCTGCAGATCAGCTGCATCGGGAAGCT  1787
                |||||||| ||     ||    ||||||  |||||||||| |||||||||||

Qy   2517  GGC  2519
           |||
Db   1788  GGC  1790
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;        PRIOR APPLICATION NUMBER: 60/241,808
;        PRIOR FILING DATE: 2000-10-20
;        PRIOR APPLICATION NUMBER: 60/241,826
;        PRIOR FILING DATE: 2000-10-20
;        PRIOR APPLICATION NUMBER: 60/241,786
;        PRIOR FILING DATE: 2000-10-20
;        PRIOR APPLICATION NUMBER: 60/241,221
;        PRIOR FILING DATE: 2000-10-20
;        PRIOR APPLICATION NUMBER: 60/226,681
;        PRIOR FILING DATE: 2000-08-22
;        PRIOR APPLICATION NUMBER: 60/246,475
;        PRIOR FILING DATE: 2000-11-08
;        PRIOR APPLICATION NUMBER: 60/225,759
;        PRIOR FILING DATE: 2000-08-14
;        PRIOR APPLICATION NUMBER: 60/225,213
;        PRIOR FILING DATE: 2000-08-14
;        PRIOR APPLICATION NUMBER: 60/231,243
;        PRIOR FILING DATE: 2000-09-08
;        PRIOR APPLICATION NUMBER: 60/233,065
;        PRIOR FILING DATE: 2000-09-14
;        PRIOR APPLICATION NUMBER: 60/227,182
;        PRIOR FILING DATE: 2000-08-22
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Query Match        16.6%;    Score 590.8;  DB 11;  Length 837;
Best Local Similarity    85.7%;    Pred. No. 9.9e-158;
Matches  655;  Conservative  1;  Mismatches  108;  Indels  0;  Gaps  0;

Qy  2735  ATGCTCAGCAGTGGAGTGACTGCCCGGCCTAGACTTCCTCTGGAAACTACAGGCAACAG 2794
               | ||||||||||||||| | ||||||||| ||||||||||||||||| ||| ||||| ||||
Db     1  ACGCCCAGCAGTGGAGTCCACTGCCCCGCCCTCGACTTCCTCTGGAGACTGCAGGCCACAG 60

Qy  2795  GGGAGAAGGAGGAGGAGGAGATCGAGGAGCTACAGGCATACAACCGGAGGCGCTGCTGCATAACATTC 2854
               |||||| || ||||||||||||||||||||||| |||||| ||||||| | ||||||||||| ||||||
Db    61  AGGAGGATAGAGAGGAGGAGGAGATCGAGGAGCTGCAGGCCTACAACCGGCGGCGCTGCTGCACAACATCC 120

Qy  2855  TGCCCAAGGACGTGGGCGCCCACTTCCTGCCCGGGAGCGCGCCAATGATGAACTCTACT 2914
               |||||||||||||||||||||  || ||||||| ||||||||| |||||||||| |||||||
Db   121  TGCCCAAGGACGTGGGCGCCGCCTCACTTCCTGGCCCGGGAGCGGGCCAATGATGAGCTCTACT 180

Qy  2915  ATCAGTCGTGTGAGTGTGGCTGTTATGTTGCCTCCATTGCCCTCGCGGCTGCTCAACGAGATCA 2974
               ||||||| ||||||| | ||| ||| | ||||||||||| ||||||||| |||||||| |||||||
Db   181  ATCAGTCCGTGAGTGTGTGGGGTCATGTTCGCCTCCATCGCCCTCGCCGCTGCTCAATGAGATCA 240

Qy  2975  ATGTGGAGCTGGAGGCAAACAATGAGGGTGTCGAGTGCCTGCGGCTGCTCAACGAGATCA 3034
               | || |||||||||||| |||||| |||||||||||||||||||||||| |||||| |||||||
Db   241  ACGTTGAGCTGGAGGCCAACAACGAGGGTGTCGAGTGCCTGCGGCTACTCAATGAGATCA 300

Qy  3035  TCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCGGGCAGCTGGAAAAGATCAAGA 3094
               |||||||||||||||||||| |||||||||||| ||||| |||||||||| ||||||||||
Db   301  TCGCTGACTTTGATGAGATCATCAGCGAGGATCGGTTCCGGCAGCTGGAGAAGATCAAGA 360

Qy  3095  CGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGG 3154
               | || || ||||||||||||||||||||| |||||||||| ||||| |||||| |||||||
Db   361  CCATCGGCGCAGCACCTACATGGCTGCCTCCGGGCTCAACGACTCTACCTACGCAAGGTGG 420

Qy  3155  GCCGCTCCCACATCACTGCCCTGGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGC 3214
               || |  |||||||||||||||||||||||| |||||||||||||||||||||||||||||| 
Db   421  GCAAGACCCACATCACTGCCCTGGCTGACTTTGCCATGAAGCTGATGGACCAGATGAAGT 480

Qy  3215  ACATCAATGAGCACTCCTTCAACAATTTCAGATGAAGATTGGGCTGAACATGGGCCCAG 3274
               |||||||||||||||||||||||||| ||| |||||||| ||||| |||||||| |||| 
Db   481  ACATCAATGAGCACTCCTTCAACAACTTCCAGATGAAGATCGGGCTCAACATCGGCCCCG 540

Qy  3275  TCGTGGCAGGTGTCATCGGGGCTCGGAAGCCACCAGTATGACATCTCGGGGAACACAGTGA 3334
               | |||||  ||||| || ||||| ||||||||  ||||| |||||||| ||| ||| |||||
Db   541  TGGTGGCCGGGGTGATAGGGGCACGAAAGCCCTCAGTACGACATCTGGGGCAATACCGTGA 600

Qy  3335  ATGTCTCTAGTCGTATGGACAGCACGCACGGGGTCCCGACCGTGACCACGGACC 3394
               | ||  | ||| || ||||||||||||||| ||| |||||||  |||| |||| |
Db   601  ACGTGGCCAGCCGCATGGACAGCACGCACCGGGTACCCGACCGCATCCAGGTCACCACAGACA 660

Qy  3395  TGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTCGAGGGTGA 3454
               |||||||||| || |||||||| |  |||||||||||||| |||| | |||
Db   661  TGTACCAGGTGCTGGCTGCCAACAGTACCAGCTGGAGTGCCGGKGCGTGGTCAAGGTCA 720

Qy  3455  AGGGCAAGGGGGAGATGACCACCTACTTCCTCAATGGGGCCCC 3498
               |||||||||||| |||||| ||||||||||||||||| |||||
Db   721  AGGGCAAGGGGCGAGATGAATGACCTACTTCCTCAATGAGAGGGCCC 764
```

RESULT 9

US-09-764-868-181
; Sequence 181, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 181
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (815)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (852)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (878)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (883)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-181

Query Match   14.9%;   Score 528.6; DB 10;   Length 915;
Best Local Similarity   85.7%;   Pred. No. 5.7e-140;
Matches 599; Conservative   0; Mismatches 99; Indels   1; Gaps   1;

Qy   2800 AAGGAGGAGAGATGGAGGAGCTACAGCATACAACCGGAGGCTGCTGCATAACATTCTGCCC 2859
                || ||||||||||||||||||| |||||| |||||||||||||| ||||| ||||||||
Db   17 AAAGAGGAGAGATGGAGGAGCTGCA-GCCTACAACCGGCGGCTGCTGCACAACATCCTGCCC 75

Qy   2860 AAGGACGTGGCGGCCCACTTCCTGCCCGGGAGCGCCCGCAATGATGAACTCTACTATCAG 2919
                ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   76 AAGGACGTGGCCGCTCACTTCCTGCCCCGCGACGCGGCGGCAATGAGTCTCTACTATCAG 135

Qy   2920 TCGTGTGAGTGTGTGGCTGTTATGTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTG 2979
                ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   136 TCCTGTGAGTGTGTGGCGGTCATGTTCGCCTCCATCGCCAACTTCTCCGAGTTCTACGTT 195

Qy   2980 GAGCTGGAGCAAACAATGAGGGTGTCAGATGCCTGCGCTGCTCAACGAGATCATCGCT 3039
                |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   196 GAGCTGGAGCAGCAAACAACCAGAGGGTGTCGAGTGCGTGTCAACGAGATCATCGCT 255

Qy   3040 GACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATT 3099
                ||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||
Db   256 GACTTTGATGAGATCATCAGCGAGGATCATCGGTTCCGGCAGCTGGAGAGATCAAGACCATC 315

Qy   3100 GGTAGCACCTACATGGCTGCCTCACGGGCTGCCTCAGGGCTGAACGCTGGCGGCCGC 3159
                ||||||||||||||||||||||||||||||||||| |||||||||||||| ||| ||
Db   316 GGCAGCACCTACATGGCTGCCTCCCGGGCCTCCGGCCTCAACGACTTCACCTACGACAAGGTGGGCAAG 375

Qy   3160 TCCCACATCACTGCCCTGCCTGACTACGCCATGCGGGCTCATGGAGCGACGATGAAGCACATC 3219
                ||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   376 ACCCACATCAAGGCACTGGCCGACTTTGCCATGAAGCTGTGATGGACCAGATGACATTGACACATC 435

Qy   3220 AATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTG 3279
                ||||||||||||||||||||||||||||||||||||| |||||||| ||||| |||||||
Db   436 AATGAGCACTCCTTCAACAACTTCCAGATGAAGATCGGGCTCAACATCGGCCCCGTGGTG 495

Qy   3280 GCAGGTGTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAACACAGTTGAATGTC 3339
                ||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db   496 GCCGGGGTGATAGGGCACGAAAGCCTCAGTACGACATCTGGGGCAATACCGTGAACGTG 555

Qy   3340 TCTAGTCGTATGGACAGCACGCGGGGGTCCCCGACCGAATCCAGGTGACCGGACCTGTAC 3399
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PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/234,997
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PRIOR APPLICATION NUMBER: 60/229,343
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PRIOR APPLICATION NUMBER: 60/229,513
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PRIOR APPLICATION NUMBER: 60/231,413
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PRIOR APPLICATION NUMBER: 60/239,935
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PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-22
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PRIOR APPLICATION NUMBER: 60/230,438
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PRIOR APPLICATION NUMBER: 60/215,135
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PRIOR FILING DATE: 2000-08-14
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PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/241,221
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PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14

Query Match   14.9%;   Score 528.6; DB 11; Length 915;
Best Local Similarity   85.7%;   Pred. No. 5.7e-140;
Matches 599; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

Qy 2800 AAGGAGGAGATGGAGGAGCTACAGGCATACACACCGGAGGCTGCTGCATAACATTCTGCCC 2859

Query Match 14.4%; Score 512.4; DB 14; Length 3518;
Best Local Similarity 49.8%; Pred. No. 4.4e-135;
Matches 1571; Conservative 0; Mismatches 1506; Indels 75; Gaps 8;

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Qy     409 GAGCGCCTGTACGACGGTACTTCTTCCAGATGAACCAGACCAGCCGACGCTGCTGATG  468
           ||| || ||||| | || |  || ||||||||||| ||||||  || || ||  ||||
Db     286 GACTCTTCTCACGAGACCTACTACAGCCTGAGCAGTACCCGCTGCTGCTGCTGCTG    345

Qy     469 GCGGTGCTGCTGCTCAGCGTGCTGCTGCGGCCGCTGCTGGGGCCGCACCCGCCCCCT  528
               |  || ||  ||  |||||||||||  |||  ||  ||    ||||
Db     346 CTGGGGATCGGTCGTGTGCGTGCTGCGGCTGGGCGCCTGGGGCCAGCCGCAGG      405

Qy     529 CAGCCTGCCTATG----------TGGCACTGTTGGCCTGTGCCGCCGCCCTGTTCGTG  576
           || ||| ||  ||          || ||| ||  ||  ||| ||  ||  || |||| |
Db     406 GAGCTGACCTCAGACCCGAGCTTCCGCTGTGCTGTGCGTGTGCGCGCGGCCTTCTCG   465

Qy     577 GGGCTCATGGTGGTGTAACCGGCATAGCTTCCGGGAGCAGCAGCTCCATGTGGTGGAGT  636
            ||| |||| ||| |     ||  | ||  ||||  ||||| |||    |||| ||  | |
Db     466 CTGCTGCTGGGCCTTCGCTTCCGGGGCGCGTCCAGGCGCCTCTCGCAGCGACACCCG    525

Qy     637 TACGTGGTGTGGGCATCGTAGGCTCATGGACGCAGCTAGGCGCACCGTCCTCCGCCGGG  696
            || |||| ||||   | |   |||   ||  |||||   | |  ||  ||  ||||||||
Db     526 GGCTTGGTATGGGTCGCGCTGCATGGAGCGCCTGTCTTTGTCTACATCGGCTACACGCTC  585

Qy     697 CGCAGCCCCTCGGGGCCTCTGGTGCCCTGTGTTCTTTGTCTACATCGGCTACACGCTC  756
           |||| || ||| ||||  || | |||   | ||| |  ||||||   ||  ||  || |
Db     586 GTGAGCGCCTGGACCAGGTGTCCATTTTCTCTTCGTCATCTTCAGCGGGCTATGCCATG   645

Qy     757 CTCCCCATCCGCATGCGGCGGCGCCGTCCTCCAGCGGCCTCCTCCACCTTGCATTTG  816
            ||| || ||| |  |||| |||  || ||  ||  || |  |  || |  || | |
Db     646 CTGCCCTTGGGCATGCGGGACGCGCCGTCGCGGGCGGCCTCGCTGCTCTCGCTCGATCTG   705

Qy     817 AT--------CTTGGCCAACTTAACCGTGGTGATGCGTGATGCCTTCCTG--GAAGCAG  864
                       ||||| || |  || |  || ||| ||||  |  ||| | |  ||| | |
Db     706 CTGGTCCTCGGGTCGTATCTTCGGGGCCGCAGCCGACCTCACGCCGCGCGCGAG      765

Qy     865 CTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAAGTCATTGGCATCTGCACCACTAT  924
           || ||||| ||  ||| ||    || |   || ||  |  ||||  ||| ||  ||||
Db     766 TTGGCAGCAAAGCAGTGCTGTCCTGTGTGTCGTGTGGGCAGGAGTGTACCACAAGGGCG   825

Qy     925 CCAGCAGAGGTGTCTCAGCGCCGGCCCTTCAGGAGCCCTTCGGAGGCCCGGTTACATC  984
           ||| | ||| || ||  ||   ||  |  || ||| |  | |||| || ||  |||||
Db     826 CTGATGGAGCGGCCCGGTCCGGGGCAGCAACTCACCTCCCTGCTGCGTGTTATTGCCCC   885

Qy     985 CTCCACCTGCAGCAATGAGATCGGACGCACATGAGAATCGGCGCTGCGTCGGTATTGCCCCAG  1044
           |||  ||  || | | |||| | || ||  | ||| | ||| |  |  ||  | ||  ||  ||
Db     886 CGGCGGCTGCAGGAAGAAGCAGCAGACCAAGAACACCTTCTCTTGTCCATCGTCGTTGTCCTGCC   945

Qy    1045 CACGTTGCCATGGAGATGAAAGAAGATCATCAACACAAAAAAGAGA----------  1091
            |  ||| ||| |||| | ||||||| || ||  |||||| |||| |
Db     946 TACCTGGCCCGAGAGATGAAGGCAGAGATCATGGCACGGCGCAGGACAGGGGTCA   1005

Qy    1092 ---------CATGATGTTCCACAAGATCTACATACAGAAGAGCATGACAATGTCAGC  1137
                     || ||| || ||||| || || |  || |||  | || || |  ||||
Db    1006 CGGGCCAGAGAGCACTAACAATTTCCACAGCCTTCATGTCAAGAGCACCAGGAGTCAGC  1065

Qy    1138 ATCCTGTTTGCAGACATTGAGGGCTTCACCAGCTCGCCATCCCAGTGCACTCCGCAGGAG  1197
            ||   || |||| ||  | | ||| ||  | ||   |   |  ||| |  ||  || | ||
Db    1066 GTGCTTGTATGCTGACATCTGGGCTTCACGCGCGGTTCCCAGCCGAGCGTTCCCTAAGGAG  1125

Qy    1198 CTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTGACAAGCTGGCTGCGGAGAATCAC  1257
            |||| | || ||  |||| |||| ||||| |  ||| || ||| ||  || || | | |
Db    1126 CTGGGTGCTCATGCTCATGAGCTCTTTGGCAAGTTCGACCAGTTCGA   1185

Qy    1258 TGGCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGGGCTGCCGAGGCC  1317
            || | ||| | ||||| |  | ||| | || || || || |  ||||   ||||  | |||
Db    1186 TGCATGCGGATCAAGATCCTCGGGGGACTGTTACTACTGTGTCTCTGGGGCTGCCACTCTCA  1245

Qy    1318 CGGGGCCGACCATGCCACTGCGTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCG  1377
            || | | |  || | |   || |||||| || |||| |||||||  || ||| |||| ||
Db    1246 CTGCCAGAGCCATGCCATCAACTGCGTGCCATGGGCGCCTGGAGAGCATGCCCGGCCATCAGG  1305
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Db      17 AAAGAGGAGGATGGAGGAGCTGCA-GCCTACAACCGGCGGCTACCACAACATCCTGCCC   75
           || |||||||||| ||||||| ||| |||  ||||||  |  || || || |||||||||
Qy    2860 AAGGACGTGGCGGCCGCTCACTTCCTGCCCGGGAGCGCCCGAATGATGAACTCTACTATCAG  2919

Db      76 AAGGACGTGGCCGCTCACTTCCTGCCCGGGAGCGCCCGAATGATGAGCTCTACTATCAG  135
           |||| |||||| || ||||||||||||| || |||||||||||||| |||||||||||
Qy    2920 TCGTGTGAGTGTGTGGGTTGTGTTATGTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTG  2979

Db     136 TCCTGTGAGTGTGTGGCGGTCATGTTCGCCTCATGCCCAACTTCTCCGAGTTCTACGTT  195
           || |||| |||||||||  || |||| |  || ||| |||||||||| |||||||| ||
Qy    2980 GAGCTGGAGGCAAACAATGAGGGTGTGCAGCAGATCATGGACCCGTAGTACAGATCATCGT  3039

Db     196 GAGCTGGAGGCCAACAACAACGAGGGTGTCGAGTGCCTGCGGCTGCTGGGGACTACTCGCT  255
           |||||||||||||| || || ||| ||||||||| | |||  || ||| | |  |||||||
Qy    3040 GACTTTGATGAGATTATCAGCGAGGAGGGTGTTCCGCAGCTGAAAAGATCAAGACGATT  3099

Db     256 GACTTTGATGAGATCATCAGCGAGGATCGGTTCCGGAGAGCTGGAGAGATCAAGAACCATC  315
           |||| ||||||| |||||||||||  |||| |||| ||||| ||||||||||| || ||
Qy    3100 GGTAGCACCTACATGGCTGCCTCAGGGTGCCAGCACCTACGATCAGGTGGGCCGC  3159

Db     316 GGCAGCACCTACATGGCTGCCTCCGGGCTTCCCGGGGCGCTCAACGACTTCACCTACGACAC  375
           || |||||||||||||||||||| |||  | |||||| | | || || ||  |||| ||
Qy    3160 TCCCACATCACTGCCCTGCTGACTACGCCATGCGGCTCATGGAGCGCAGAGCACATC  3219

Db     376 ACCCACATCACTGCCCTGCTGACTGCCCGGACCTTTGCCTATGAAGCTGATGGACCAGATGAGTACATC  435
           ||||| ||||||||| |||||||| |||| || | ||| || ||| |||| || ||  |||||||
Qy    3220 AATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGCTGAACATGGGCCCCAGTCGTG  3279

Db     436 AATGAGCACTCCTTCAACAACTTCCAGATGAAGATCGGGCTCAACATCGCCCCCGTGGTG  495
           ||||||||||||||||||| ||||||||||||||| |   ||||||| |||||| |||||
Qy    3280 GCAGGTGTGTCATCGGGGCTTCGGAAGCCACAAGTATGACATCGGGGAACACAGTGAATGTC  3339

Db     496 GCCGGGGGTGATAGGGGACACGAAAGCCTCAGTACGACCATCTGGGGCAATACCGTGAACGTG  555
           || ||| ||||  ||| || | ||||| |||||   |  |||||||  ||| |||| | |||
Qy    3340 TCTAGTCGTATGGACAGCAGCAGGGGGTCCCGACCTGTAGGTGACCACCGTGACCCTGTAC  3399

Db     556 GCCAGCCAGGACAGCAGCAGCCGTGGTCGTACCGGACCATCCAGGTCACCACAGACATGTAC  615
           || || ||||||| |||| |||| || |||||||| ||||||| |||| || |||||||||
Qy    3400 CAGGTTCTAGCTGCTGCAAGGGGCTACCAGCTGGAGGTGTCGAGTGTGGTCAAGGTCGAAGGGC  3459

Db     616 CAGGTGCTGCTGCCAACACTACCAGCTGGAGGTGTCGGAGTGCCGGGGGTCGTGGTCAAGGTCAAGGGC  675
           |||| |||||||||||||| ||||||||||||||||| || |  || |||  |||| ||||||||||||
Qy    3460 AAGGGGGAGATGACAACTACTTCCTCAATGGGGCCCCC  3498

Db     676 AAAGGCGAGATGATGACCTACTTCCTCAATGGAGGGCCC  714
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RESULT 11

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Db   2383 CTGCCTCTCATCAGTGCTCCCATACTCCATGCACTGCTGCACGCTGGGCTTCCTCTCTGC 2442
Qy   2515 TTGGCCATGATCTTTGTCTTGGGCTCATCTATTTGGTGCTGCTTCGTGCTGGCTCCCCCA 2574
Db   2443 TCCCTCTTTCTGCACATGAGCTTCGAGCTGAAGCTGCTGCTCCTGCTGTGCTGGCTGGCG 2502
Qy   2575 GCCACCATCTTTGACAACTATGACCTACTCTGCTTGGCGTCATGGCTTGGCTCTTCCAAT 2634
Db   2503 GCATCCTGCTCCTCTTCCTGCACTCCCATGCCTGCTGTGTCGGAATGCCTCATCGTCGC 2562
Qy   2635 GAGACCTTTGATGGGCTGGACTGTCCAGCTGCTGCAGGAGGGTGGCCCTCAAATATATGACC 2694
Db   2563 CTCTATCTGGGCCCCTTGGACTCCAGGCCCGAGTGCTGAAGGAGCCCAAACTGATGGGT 2622
Qy   2695 CCTGTGATTCTGCTGTGTTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTCG 2754
Db   2623 GCTATCCTCCTTCTCATCTTCCTGGAAGAGAAGCTGAGGAGGAGGAGGAGGAGTAC 2682
Qy   2755 ACTGCCCGGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGAAGGAGATGGAG 2814
Db   2683 TACTGCGCGTCCTGTGGAGAAGAAGCTGAGGCAGGAGGAGGAGGAGCAGAG 2742
Qy   2815 GAGCTACAGGCATACAACCGAGGCGCGCAATAACATTCTGCCCAAGGACTGGCGGCC 2874
Db   2743 ACGATGGAGACCTGACTCGGCTCGTCTTGGAGAACGTGCTTCCCTGCCACAGTGGCCCCC 2802
Qy   2875 CACTTCCTGGCCCGGAGCGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTG 2934
Db   2803 CAGTTCATTGGCCAGAACCGGCGCCAACCGGATCCTCACCAGTCCTATGAATGCGTT 2862
Qy   2935 GCTGTTATGTTGCCTCCATTGCCAACTTCTCTGAGTTCTCATGTGAGGCTGAGGCAAAC 2994
Db   2863 TGTGTCCTCTTCGCTCCGCCTCAGTCCCAGACTTCAAGGAGTTCTACTCTGAATCCAACATCAAT 2922
Qy   2995 AATGAGGGTGTCGAGGCGCTTGCGAGCTGTCAACGAGCATCGCTGCACTTTGATGAGATT 3054
Db   2923 CATGAGACGGCCTAGAGTGTCTGAGGCTGCTCAATGCATAATTGCTGATTTTGATGAGCTG 2982
Qy   3055 ATCAGCGAGGAGCGCGGTTCCGGCAGCTGGAAAAGATCAAGACCATTGGTAGCACCTACATG 3114
Db   2983 CTCTCCAAGCCCAAGTTCAGTTGGGGTGGAGAAGATCAAGACCATCGGCACCACCTACATG 3042
Qy   3115 GCTGCCTCAGGGCTGAACGGCCAGCAC--------------CTACGATCAGGTGGGC 3156
Db   3043 GCAGCCACAGGTTAAATGCCACCTCTGGACAGGATGCACAACAGGATGCTGAACGGAGC 3102
Qy   3157 CGCTCCCCACATCACTGCCCTGCTGACTACGGCCATGAGCAGCATGAGAGCAC 3216
Db   3103 TGCAGCCACCTTGGCACTATGGTGAATTTGCCGTGGCCCGTCTAAGCTGGACGTC 3162
Qy   3217 ATCAATGAGCACTCCTCAACAATTTCAGATGAACAATTCGGGGCTGAACATGGCCCAGTC 3276
Db   3163 ATCAACAAGCATTCATTCATTCAACCAACTTCGCCTCGGAGTGGTTGAACCATGGACCCGTA 3222
Qy   3277 GTGGCAGGTGTCATCGGGGTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAAT 3336
Db   3223 GTAGCTGGAGTTATTGGGGCCCAGGAGCCGCAATATGACATTTGGGCAACACAGTGAAC 3282
Qy   3337 GTCTCTAGTGTATGGAACGCGATAGCAGCGGGGTCCCCGACCAGGTCGGACCACCGACCCTG 3396
Db   3283 GTGGGCCAGCCGCATGGAGCATAGCAGCAGTACCAAAATCCAAGTGACTGAGGAGACA 3342
Qy   3397 TACCAGGTTCTAGCTGCCAAGGGCTACCAGGCTGGAGTGTCAAGGTGAAG 3456
Db   3343 GCATGGCCCTACCAGTCCCTGGGCTACCACCTGCTACACCTGCTGCCTCAGGGGTGTCATCGGGGTCATCAAGGTGAAA 3402
Qy   3457 GGCAAGGGGGAGATGACCCACCTACTTCCTCAA 3488
Db   3403 GGCAAAGGGCAGCTCTGCACCTACTTCCTGAA 3434
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RESULT 12

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Qy   1378 CTGGTACGTGAGGTGACAGAGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGC 1437
Db   1306 AAACTGCGGGCAGCCAGCCACTGGCGGCTGGCTTGGGCATCAACATGCGTGTGGGCCAGC 1365
Qy   1438 GTGCACTGCGGCGTCCTTGGTTGCCGAAATGGCAGTTCGATGTGGTCAATGATGTG 1497
Db   1366 GTACTGTGTGGGAGTCATCGGGCTGCAGGACGCGTTTGGTCACATGATGTC 1425
Qy   1498 ACCCTGGCCAACCACATGCGAGCGAGGAGGCCGGCGCCCGGCCTGCCGCCATCCACATCACTACTGGGCA 1557
Db   1426 ACACTGGCTAACCACCATATGGAGCCACATGGAAGCGAGTGCACATCACAGGGCT 1485
Qy   1558 ACACTGCAGTACCTGACAGGGGACTACGAGGTGGAGCCAGGCCGTGTGGCGGCCAAC 1617
Db   1486 ACCCTGGCCCCTGGCAGGGGCTTATGCTGTGGAGGACGCAGGCATCGGGAC 1545
Qy   1618 GCGTACCTCAAGGAGCACCATTGAGACTTCCTCATCCTGGGCGCCAGCCAGAAACGG 1677
Db   1546 CCCTACCTTCGGGAGCTAGGGGAGGGCTTATGCTGTCATCGATCCAGGGGCAGAGGAG 1605
Qy   1678 AAAGAGGAGAGGCCATGCTGCTGCAAGCTGCAGCGGACTGGGTTCCTGCCTTCCCCGGA 1737
Db   1606 GAGGATGAGAGAGGGGCACTGGAGGCTTGCTGTCTCCGCGACTCCAAGGAGATGCGT 1665
Qy   1738 CTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCCCCGGACCAAGGACTCCAAGGCCTTC 1797
Db   1666 CCATCACTGCTGATGACCGTTACCTGGAGTCCTGGGGGGGCAGCCAGCCAAGCCTTTGCCCAC 1725
Qy   1798 CGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCGGGCGCACCCAAGATGCCCTG--A 1855
Db   1726 CTGAGCCACGGAGAACAGCCCTGTGTCCACCTTCCCCGGAGAACGAACCCCTGGCT 1785
Qy   1856 ACCCTGAGGATGAGGTGGA-TGAGTTCCTGAGCCGTGGCATCGATGCCCCGCAGCATTGAT 1914
Db   1786 TCCTTCAGCACCCAGTGGAGCCTGGATCGGAGCCCGTACCCCCGGGACTAGATGATGAA 1845
Qy   1915 CAGCTGCGGAAGGACCATGTGCGCCGGTTCTGCGCTCACCTTCCAGAGAGAGGATCTTGAG 1974
Db   1846 CTGGACACCCGGGGGATGCCAAGTTCTTCTCCAGTGTTCATTGAGCAGTCCAACTCGCAGAAACAG 1905
Qy   1975 AAGAAGTACTTCCCGGAAGGTGATCCCCGCTTGATCCCTGCCTGTGCCGTGTTG 2034
Db   1906 TGGAAGCAGTCGAAGGACTTCAACCCACTGACACTTCAGAGAGAAGAGAGATGGAG 1965
Qy   2035 GTCTTCTGCTTCATCTGCTTCATCAGCTTCATCTTCCCACACTTCCCACCCTGATGCTT 2094
Db   1966 AAAGAGTACCGACTCTCTGCAATCCCGCCTTCAAATACTATGAGAGCCTGCACCTTCCTG 2025
Qy   2095 CAGCTGCGGAAGGACACCATGTGCGCCGGTTCTGCGCCTAATCGTGCTGTGTAC 2154
Db   2026 GTTTTTCTCTCAACTTCATCATCCAGATGGCCTGCAGCTCAGTGTGACAAACAGCCCCAGCTCTGGCC 2085
Qy   2155 TCCTGTGGTTCTCTGTTCCCTAAGGCCCTGCAACGTGTTGCCTGTGCCGCTCA 2214
Db   2086 ATCAC---GTATAGACATCACTTTCCTCTCTTTTTGTGTGCTCTCTCA 2142
Qy   2215 CGGGCCACACTAGCACCGCAGTTGGCATCTCTTTCGTGTGTTTACTTCTGCCATT 2274
Db   2143 GAGGACCTGATGAGGTGTGCCTGAAAGGCCCCAAGATGCTGCCTGCACTCTG 2202
Qy   2275 GCCAACATGTCACCTGTAACCACACACCCATACGGAGCTGTCAGCCCGATGCTGAAT 2334
Db   2203 TCTGGCCTGGCCACAGCAGACCAGGACTAGCCTTGGGACACCGCCACCATCCTC 2262
Qy   2335 TTAAACCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTTCTCTGGGCCTG 2394
Db   2263 CTTGTCTTTGCCATGTGCATTACCAGCTGTGTTCTTCTTCCCAAACATCATCAGACTGCCCT 2322
Qy   2395 GATGCTCCCCTGTGTGAGGGCACCATGCCAGTTTCCTCAGAGTACTTCATCGGG 2454
Db   2323 TTCCAAGCTCCCAATGTGTCCCATGATTTCCAACCTCTCCTGGGAGCTCCCTGGGTCT 2382
Qy   2455 AACATCTGCTGAGTCTTGCGCCAGCTCGTTCTCCTGCACATCAGCAGCATCGGGAAG 2514
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US-10-282-942-1
; Sequence 1, Application US/10282942
; Publication No. US20030087295A1
; GENERAL INFORMATION:
;  APPLICANT: Silos-Santiago, Inmaculada
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PAIN DISORDERS USING 9805
;  FILE REFERENCE: MPI01-240P1RM
;  CURRENT APPLICATION NUMBER: US/10/282,942
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,047
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6196
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-282-942-1

  Query Match              13.9%;  Score 493;  DB 15;  Length 6196;
  Best Local Similarity    49.8%;  Pred. No. 1.9e-129;
  Matches 1586;  Conservative    0;  Mismatches 1515;  Indels   84;  Gaps   10;

Qy         417 GTACCAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGCGGTGCT 476
               ||||||||    |  |   ||   |   | |     |  |   |||||| |||| |
Db         337 GTACCAGCTCACCAGCCAGCATGGGCCGCTGCTGCTCACGCTCCTGCTGGTGGCCGCCAC 396

Qy         477 GGTGCTGCTCACAGCGGTGCTGCTGGCTTTCCACGCCGCACCCGCCCGCCCTCAGCCTGC 536
                |      |  |     |  |  | || |||  |   |    | ||  |   || |  ||
Db         397 TGCCTGCGTGGCCCTCATCATCATTGCCTTCAGCCAGGGGGACCCCTCCAGACACCAGGC 456

Qy         537 CTATGTGGCACTGTTGGCCTGTGCCGCCGCCCTGTTCGTGGGGCTCATGGTGGTGTGTAA 596
               |  | |||   ||  |  |   |     ||  |||| | ||  |||   ||| ||    |
Db         457 CATTCTGGGCATGGCGTTCCTGGTGCTGGCGGTGTTTGCGGCCCTCTCTGTGCTGATGTA 516

Qy         597 CCGGCATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGTTACGTGGTGCTGGGCATCCT 656
               |    |  |  |||  | |  ||   |  |||   ||       |      || |  | |
Db         517 CGTCGAGTGTCTCCTGCGGCGCTGGCTCAGGGCCTTGGCGCTGCTCACCTGGGCCTGCTT 576

Qy         657 GGCGGCAGTGCAGGTCGGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCCTCTGCG-GGCC 715
               || |||  ||      | |   |   |||  |||    |        ||| ||||  ||
Db         577 GGTGGCGCTGGGCTATGTGCTGGTGTTCGACGCATGGACAAAGGCGGCCTGTGCGTGGGA 636

Qy         716 TCTGGTGCCCT-----GTGTTCTTTGTCTACATCGCCTACACGCTCCTCCCCATCCGCAT 770
                | ||||||||      ||||| |||||| | | |  ||||| || || ||| || ||||
Db         637 GCAGGTGCCCTTCTTCCTGTTCATTGTCTTCGTGGTGTACACACTACTGCCCTTCAGCAT 696

Qy         771 GCGGGCTGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCA 830
               |||||  || |||  |   ||    | |  | |  |||  ||  |  |  ||  | |
Db         697 GCGGGGCGCTGTCGCCGTTGGGGCCGTCTCCACTGCCTCCCACCTCCTGGTGCTCGGTTC 756

Qy         831 ACTTAACCGTGG------------TGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGT 878
                 | |   | ||               || |    |  ||  ||||||    ||||| |
Db         757 TTTGATGGGAGGCTTCACGACACCCAGTGTCCGGGTGGGGCTGCAGCTGCTGGCCAACGC 816

Qy         879 GCTGCTGTTCCTCTGCACCAACGTCATTGGCATCTGCACACACTATCCAGCAGAGGTGTC 938
                 |  | |||||| ||    ||| | |  |||  || |    |  | | |    |||   |
Db         817 AGTCATCTTCCTGTGTGGGAACCTGACAGGCGCCTTCCACAAGCACCAAATGCAGGATGC 876

Qy         939 TCAGCGCCAGGCCTTTCAGGAGACCCGCGGTTACATCCAGGCCCGGCTCCACCTGCAGCA 998
                   ||  |   |||     | ||       | |||||||  ||| |   | ||||
Db         877 GTCCCGGGACCTCTTCACCTACACTGTGAAGTGCATCCAGATCCGCCGGAAGCTGCGCAT 936

Qy         999 TGAGAATCGGCAGCAGGAGCGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGA 1058
                ||||| || |||||||||   ||||||||||| ||  | ||    ||| |  ||||||
Db         937 CGAGAAGCGCCAGCAGGAGAACCTGCTGCTGTCAGTGCTTCCGGCCCACATCTCCATGGG 996

Qy        1059 GATGAAAGAAGACATCAACACAAAAAAAGAA---------------------------GA 1091
                |||||    | ||||| |  |       |                            ||
Db         997 CATGAAGCTGGCCATCATCGAACGGCTCAAGGAGCATGGTGACCGTCGCTGCATGCCTGA 1056

Qy        1092 CATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGA 1151
               ||  |  |||||||   ||||| |  ||| |||  | |||||||||||||| | ||| ||
Db        1057 CAACAACTTCCACAGCCTCTACGTCAAGAGGCACCAGAATGTCAGCATCCTCTATGCGGA 1116

Qy        1152 CATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGAGCTGGTCATGACCCT 1211
               ||| | |||||||||    |||||   | | ||  || |  ||||||||||  ||   ||
Db        1117 CATCGTGGGCTTCACGCAGCTGGCCAGCGACTGTTCTCCCAAGGAGCTGGTGGTGGTGCT 1176

Qy        1212 GAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATCAA 1271
               |||||||||||||| |  ||| ||| || | ||   ||  ||  | ||| || | |||||
Db        1177 GAATGAGCTCTTTGGCAAGTTCGACCAGATCGCCAAGGCCAACGAGTGCATGCGAATCAA 1236

Qy        1272 GATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCATGC 1331
               |||| | || ||||| ||||||||||| || || ||||| | | | | | |   ||| ||
Db        1237 GATCCTCGGCGACTGCTACTACTGTGTATCGGGCCTGCCCGTGTCGCTGCCTACCCACGC 1296

Qy        1332 CCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGT 1391
               ||    ||| ||| |||||||| | ||||||    ||||||||  || ||| || ||||
Db        1297 CCGGAACTGCGTGAAGATGGGGCTGGACATGTGCCAGGCCATCAAGCAGGTGCGGGAGGC 1356

Qy        1392 GACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGCGT 1451
                || || ||| |  | ||||||||| |||||||| |||   |||   ||||  ||||| ||
Db        1357 CACGGGCGTGGACATCAACATGCGTGTGGGCATACACTCGGGGAATGTGCTGTGCGGGGT 1416

Qy        1452 CCTTGGCTTGCGGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGACCCTGGCCAACCA 1511
               | | ||  |||| || |||||||  || ||||||||| | || ||| ||||||||||||
Db        1417 CATCGGGCTGCGCAAGTGGCAGTATGACGTGTGGTCCCACGACGTGTCCCTGGCCAACCG 1476

Qy        1512 CATGGAGGCAGGAGGCCGGGCTGGCCGCATCCACATCACTCGGGCAACACTGCAGTACCT 1571
                ||||||||||  ||     | |||||  | ||||||||   ||| || ||  || ||||
Db        1477 GATGGAGGCAGCCGGAGTACCCGGCCGGGTGCACATCACGGAGGCCACGCTAAAGCACCT 1536

Qy        1572 GAACGGGGACTACGAGGTGGAGCCAGGCCGTGGTGGCGAGCGCAACGCGTACCTCAAGGA 1631
               | ||  ||  ||||||||||||   || |  ||     ||||  || | |||||||||||
Db        1537 GGACAAGGCGTACGAGGTGGAGGATGGGCACGGGCAGCAGCGGGACCCCTACCTCAAGGA 1596

Qy        1632 GCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCAGAAACGGAAAGAGGAGAAGGC 1691
               |  | ||||    || | |||  || | | | || |     | | |  |     |
Db        1597 GATGAACATCCGCACCTACCTGGTCATCGACCCCCGGAGCCAGCAGCCACCCCCGCCCAG 1656

Qy        1692 CATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGCTG 1751
               |   |    |     ||    |      ||   |   | |    ||  |     ||||
Db        1657 CCAACACCTCCCCAGGCCCAAGGGGGACGCGGCCCTGAAGATGCGGGCGTCAGTGCGCAT 1716

Qy        1752 GGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCAT 1811
               |   |   | |  |  | ||   || |        ||   ||    | | |     |
Db        1717 GACCCGGTACCTCGAGTCCTGGGGGGCGGCACGGCCCTTTGCACATCTCAACCACCGTGA 1776

Qy        1812 TGATGATTCCAGCAAAGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGT 1871
                   |    |||    || | ||  | | || | |       |         | |
Db        1777 GAGCGTGAGCAGTGGTGAGACCCACGTCCCCAACGGGCGGAGGCCTAAGAGCGTTCCCCA 1836

Qy        1872 GGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTGCGGAAGGACCA 1931
               |    |   || || ||  | ||          |  ||  |  | |  |  | | |||
Db        1837 GCGCCACCGCCGGACCCCAGACAGAAGCATGTCCCCCAAGGGGCGGTCGGAGGATGACTC 1896

Qy        1932 TGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAAGAAGTACTCCCGGAA 1991
                             ||||  |   |      | |         | || |  || | |
Db        1897 GTACGATGACGAGATGCTGTCAGCCATTGAGGGGCTCAGCTCCACGAGGCCCTGCTGCTC 1956

Qy        1992 GGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGTCTTCTGCTTCATCTG 2051
                  |        ||||    |||  |   ||     ||||  |     ||       |
Db        1957 CAAGTCCGATGACTTCTACACCTTTGGGTCCATCTTCCTGGAGAAGGGCTTTGAGCGCGA 2016

Qy        2052 CTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATGCTTGGGATCTATGCCAGCAT 2111
                | |  || |   | ||||  ||    |  |  |    |     |   |      | | |
Db        2017 GTACCGCCTGGCACCCATCCCCCGGGCCCGCCACGACTTTGCCTGCGCCAGCCTGATCTT 2076

Qy        2112 CTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTT 2171
               | ||    | |||||  ||   || ||| ||    |   |    |  |    |   |||
Db        2077 CGTCTGCATCCTGCTCGTCCATGTCCTGCTCATGCCCAGGACGGC--GGCACTGGGTGTG 2134

Qy        2172 CCCTAAGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGC 2231
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RESULT 13
US-09-960-706-635
; Sequence 635, Application US/09960706
; Publication No. US2003013280A1
; GENERAL INFORMATION:
;  APPLICANT: Munger, William E.
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
;  TITLE OF INVENTION: Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-01US
;  CURRENT APPLICATION NUMBER: US/09/960,706
;  CURRENT FILING DATE:   2001-09-24
;  PRIOR APPLICATION NUMBER: 60/223,323
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 09/873,319
;  PRIOR FILING DATE: 2001-06-05
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
;  LENGTH: 2731
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: Genbank Accession No. US2003013280A1 L05500
US-09-960-706-635

Query Match             12.8%;   Score 456.2;   DB 13;   Length 2731;
Best Local Similarity   52.8%;   Pred. No. 4.2e-119;
Matches 1274;   Conservative   0;   Mismatches 1023;   Indels 114;   Gaps  9;
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[Sequence alignment blocks — paired Query (Qy) / Database (Db) nucleotide rows with coordinate numbers, e.g.:]

Qy 1090 GACATGATGTTCCACAGATCTACATACAGAAGCATGACAATGTCAGCATCCTGTTTGCA 1149
Db   24 GAGAGGAATTTCCACAAGATTACATCCAGAGCACGACACAATGTGAGCATCCTGTTTGCT   83
Qy 1150 GACATTGAGGGCTTCACCAGCTGCAGGGTAGACATGGGGTAGACATGATTGAGGGGTCATGACC 1209
Db   84 GACATCTGGGTTTCACGGGTTGGCATCCCAGTGCACAGCCCAGGAGCTGGTGAAACTC 143
Qy 1210 CTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGCCTGAGGATC 1269
Db 144 CTCAAATGAGCTCTTCGGCAAGTTCGATGAATTCGCTGCGCCGCATC 203
Qy 1270 AAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGTGTCAGGGCCGACCAT 1329
Db 204 AAGATTCTCGGGGACTGCTACTACTGCGTGTCGGGCCTCACCCAGCCCAAGACTGACCAT 263
Qy 1330 GCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGGGTACGTGAG 1389
Db 264 GCCCACTGCTGTGTGGAGTGAGTTCAGCATCGCCCTGATGAGTAAGCTGACCGGCATCAACACAG 323
Qy 1390 GTGACAGGTGTGAATGTGAACATGCGCGTGCGGCATCCACAGCGGCGCGTGCACTGCGGC 1449
Db 3205 GCACTCCTTCAACTCCTTCCGCCTCCGGCATAAACCATGGGCGTGTGATTGCTGG 3264

[Additional alignment blocks continue above in the upper portion of the page:]

Db 2135 TCCTTCGGGCTGGTGGCCTGTGTACTGGGGC-TGGTGCTGGGCCTGTGCTTTGCCACCAA 2193
Qy 2232 AGTTGGCATCTTTTCCGTCCTGTGTTTACTTCTGCCAACATGTTCACCTG 2291
Db 2194 GTTCTCGAGGTGCTGCCCAGCTCGGGGGACGCTCTTGCACTATCTCTGAGAGGGTGAGAC 2253
Qy 2292 TAACCACCCCCATACGGAGCTGTGCAGCCCGA---------TGCTGAATTTAAC 2339
Db 2254 ACAGCCCCTGCTGAGGCTGACCCCTGGCCGTCCTGACCATCGGCAGCCTGCTGCACTCTGGC 2313
Qy 2340 ACCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTTCTGTGGGCCTGATGC 2399
Db 2314 CATCATCAACCTGCCCCTGATGCCTTTCAAGTTCCAGAGCTGCCTGTTGCCAATGAGAC 2373
Qy 2400 TCCCCTGTGTGAGGGCACCATGCCCACCTGCCAGCTTTCCTGAGTACTTCATCGGGAACAT 2459
Db 2374 AGGCCTACTGCCGCGCAGCAGCAAGAACAAGAGCCCTGTGTGAGCCCCTCCGTACTACAC 2433
Qy 2460 GCTGCTGAGTCTCTTGCCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGC 2519
Db 2434 CTGCAGCTGTGTCCTCGGGCTTCATCGCCTGCTGGTCTTCGGATGCATGAGCCTGGAGCC 2493
Qy 2520 CATGATCTTTGTCTTTGGGGCTTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCAGCCAC 2579
Db 2494 AAAGGTTGTGCTGCTGACAGTTGGCCCCTGGTGCCTACCTGGTCTCTTCAACCTCTCCCC 2553
Qy 2580 CATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCTTCCAATGAGAC 2639
Db 2554 ATGCTGGCAGTGGGACTGCTGTCGCGGCCAAGGCCTGGGCAACCTCACCAGCCCACGGCAC 2613
Qy 2640 CTTTGATGGGCTGGACTGTCCAGCTCGCAGGGAGGGGTGGCCCTCAAATATATGACCCCTGT 2699
Db 2614 CACCAGTGG------CACCCCTAGCTGTTCCTGGAAGGACCTGAAGACCATGACCAATTT 2667
Qy 2700 GATTCTGCTGGTGTTTGCGCGTGGCGCGTGTATCTGCATGCTCAGCAGGTGGAGTCGACTGC 2759
Db 2668 CTACCTGGTCCTGTTCTTCTACATCACCCTGCTTACACTCTCCAGACAGCAGATTGACTATTACTG 2727
Qy 2760 CCGCCTCAGACTTCCTCTGGAAACTTCCTCTGGAAGATACAGGCAACAGGGGAGGAGGATGGAGGAGCT 2819
Db 2728 CCGCTTGGACTGCCTATGGAAGAAGAAGTTCAAGAGGAGCACGAGGAGGTTTGACACCAT 2787
Qy 2820 ACAGGCATACACAACCGGAGGCTGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGGCCCCACTT 2879
Db 2788 GGGAAACGTGAACCGCCTTCTTCTTCTGAGGAACGTGTCCTGCCAGCCCACGTGGCTGCCCACTT 2847
Qy 2880 CCTGGCCCGGGAGCCGGCGCCGCAATGATGAAACTTCTACTATCAGTCGTCGTGTGAGTGTGGCTGT 2939
Db 2848 TATCG---GTGACAAGTAAACGAGGACTGGTACCATCAGTCCTATGACTGCGTCTGTGT 2904
Qy 2940 TATGTTTTGCCTCCATTGCCAACTTCTCTGAGTCTCATGTGGAGCTGGAGCGCAAACAATGA 2999
Db 2905 CATGTTTGCCTCCGTGCCGGACTTCAAAGTGTTCTACACAGAGTGCGATGTCACACAAAGA 2964
Qy 3000 GGGTGTGCAGTGCGCTCGCGGCTTCAACGAGATCATCGCTGACTTTGATGAGATTATCGCG 3059
Db 2965 AGGGCTGGAGTGCCTACGCGTCCTGCTCAATGAGATCATTGCCGACTTCGACAGCTTCCTACT 3024
Qy 3060 CGAGAGCGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGC 3119
Db 3025 GAAGCCCAAGTTCAGGCGGCGTTGGAGAGATCAAGACCATCGGCAGCACGTACATGGCAGC 3084
Qy 3120 CTCAGGGCT---------GAACGCGCAGCACCTACGATCCAGGTGGGCCGGCCGCTCCCA 3164
Db 3085 TGCAGGGCTTCAGCGTGCTCAGCGTGCGCCTCAGCGGCACGAGACCAGGAGCTGGAGCCGCATGCCCA 3144
Qy 3165 CATCACTGCCCCTGGCTGACTACGCCAATGCGGCTCATGGAGCAGATGAAGCACATCAATGA 3224
Db 3145 CATTGGTGTCATGGTGAGTTCAGCATCGCCCTGATGAGTAAGCTGGCCATCAACACAG 3204
Qy 3225 GCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCGTGGCATCCACAGCGGCAGG 3284
Db 3205 GCACTCCTTCAACTCCTTCCGCCTCCGGCATAAACCATGGGCGTGTGATTGCTGG 3264

Qy 3285 TGTCATCGGGGTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAG 3344
Db 3265 AGTGATTGGGGTCGGGGCGAAAACCTCAGTATGACATCTGGGAAAACACTGTCAATGTGGCCAG 3324
Qy 3345 TCGTATGGACAGCACGGGGGTCCCGACCAGTGACCAGGTTCCCAGTGACCAGGTTACCAGGT 3404
Db 3325 CCGAATGGAAAGCACTTGGAGAACTTGGGAAAATCCAGTTACCGAGAGAGACCTGCACCAT 3384
Qy 3405 TCTAGCTGCCAAGGGCTACCAGCTGAGGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGG 3464
Db 3385 CCTCCAGGGCCTGGTACTCTTGTGTGGAATGCCGTGGCCGTGATCAACGTCAAAGGCAAAGG 3444
Qy 3465 GGAGATGACCACCTACTTCCTCAATGGGGCCCAGCAGTAACAGGGCCCAGCCACAAA 3524
Db 3445 CCAGCTGAGGACTTACTTTGTCTGTACGGACACTGCCAAGTTTCAGGGGCTGGGGCTGAA 3504

Qy 3525 TTCAG 3529
Db 3505 CTGAG 3509

(Page contains dense DNA sequence alignment data arranged in two columns of Qy/Db paired rows with BLAST-style match bars.)

Left column (reading down, Db/Qy/Db rows with flanking position numbers):

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Db  324  GCCACCGAGGTGGATCTGAACATGCGTGTGGGTCTGCACACGGGCAGGGTTCCTCTGTGGT  383
Qy 1450  GTCCTTGGCTTGCGGAAATGGCAGTTCGATGTGTTCCAATGATGTGACCTGCCAAC      1509
Db  384  GTCCTGGGCTTGCGCAAGTGGCAGTTACGACGTGTGGTCCAATGATGTGACCTTGGCCAAT 443
Qy 1510  CACATGGAGGCAGGAGCCGGGCTGGCCGCATCCACATACTCGGCGCAACACTGCAGTAC   1569
Db  444  GTCATGGAAGCCGCTGGCCTGCCCAGGAAGGTTCATATCACAAGACGACGCCCTAGCGTGC 503
Qy 1570  CTGAACGGGGACTACGAGGTGGAGCCAGGCCGTCGTGGCGAGCGCAACGGGTCACTCAAG  1629
Db  504  TTGAATGGGACTACGAGGTAGAACCGGGTTACGGACAATGAGAGGAACAGTTTCTTGAAA  563
Qy 1630  GAGCAGCACATTGAGACTTTCCTCATCCTCGGCCGCCAGCCAGAAACGGAAAGAGGAGAAG 1689
Db  564  ACTCATAACATCGAAACCTTTTTTTATTGTGCCATCCATCCGCCAAAGATATTTCCAGGC  623
Qy 1690  GCCATGCTCGGCCAAGCTGCGAGCGGACTCGGGCCAACTCCATGGAAGGGGTGATGCCGCC  1749
Db  624  CTGATTCTTCTCAGATATAAAACC-----GGCCAAAAGGATGAAGTTCAAGACTGTCTGC   677
Qy 1750  TGGGGTTCCTGATCGTGCTTCTCCCGGACCAAGGACTCCAAGGCCTTCGGCCGGATGGGC   1809
Db  678  TACCTGCTCGTGCAGCTCATGCACTGCCGGCGAAAATGTTCAAGGCCGAGATCCCCTTCTCC  737
Qy 1810  ATTGATGATTCCAGCAAAGACAACAACGGGGACACCGGGCACCCAAGATGCCCTGAGGATGAG  1869
Db  738  AATGTCATGACCTGCGAGGACGA----------------TGACAAGCCGGAGGGC       775
Qy 1870  GTGGATGAGTTCCTGAGCCGTGCCATCGAATGCCGCAGCATTGATCAGCTGCGGAAGGAC  1929
Db  776  ATTAAGAACAGCCTCGGAAAAACTCAGAAACCGCTCATCTTTTCTACCAACG--------   828
Qy 1930  CATGTGCGGCCGGTTTCTGCTCACCTTCGAGAGAGGATCTTGAGAAGAAGTACTCCCGG  1989
Db  829  --------------TTGTCTACACACCACCCGGGCACTCGGCGTCAACAGGTACATCAGCCGC  875
Qy 1990  AAGGTGGATCCCCGCTTCGGACGTTGCGCTGCCTGCGCCCCTGGTCTCTGCTTCATC  2049
Db  876  CTCTTAGAGCCCCGCCAGACAG---AGCTGGAGATGGCAGACCTGAACTTCTTTTACCCCTG   932
Qy 2050  TGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCTGATGCGTTGGGATTCATGCCAGC  2109
Db  933  AGTAGACAAACATGTCGAACGGAGGGAGCAAAAGTACCACCAGCTTCAGGACGAGTATTTCACC  992
Qy 2110  ATCTTCCTGCTGCTGCTATAATCACCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTG  2169
Db  993  AGGCGCCGGTTGTCCTCACCCTCATCCTGCCTTATTTGGCCTTGTCTCACCTTCTAATA  1052
Qy 2170  TTCCCTAAGGCCCTGCCAACGTCGTCTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACC  2229
Db 1053  TTCCCACAGAGTGTGGTCGTCGTCCTGCTCCTGCTCTGCTGTGTTACTCTGCATCGTGCTTCCTGGTGGCC  1112
Qy 2230  GCAGTTGGCATCTTTTCCGTCCTGCTGTCGTGTGTTTACTTCTGCCATTGCCAACATGTTCACC  2289
Db 1113  TGTGTCCTGTACCTGCACACATCACCCGGGT---------CCAGTGTTTTTCCAGGGGTGCC  1161
Qy 2290  TGTAACCACACCCCCCATACGGAGCTGTGTGCAGCCCGATGCTGAATTTAACACCTGCTGAC  2349
Db 1162  TGACGATTCAGATTCGCACTGTCCTCCATCCTGGTCTGTATTTTCATAGTGGTCTTAATCTCACTCAGTAG  1221
Qy 2350  ATCACTGCTGCCACCTGGTCATCCTGCAGCTCAATTACTCCTCTGGGATGCTCCCCCTGTGT  2409
Db 1222  CCCAAGG--------TTGTGTGGGGCTGCCTGCCTGGGGCTGCCGAGCT--CCAAGCCC  1271
Qy 2410  GAGGGCACCCATGCCCACCTGCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGT  2469
Db 1272  AACAGTTCCCTGTGGTGTCCTTTCGTTCCTCTGGGGGGCCAGCGCACCAGCCCTGCCCC  1331
Qy 2470  CTCTTGGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGAAGTTGGCCATGATCTTT  2529
Db 1332  TGCCAGTCTACACACCATGCCCTGCCTCTGCGCTGGTGGGCACCCTCCCCGCTAGCCATA  1391
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Right column:

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Db  2530  GTCTTGGGGCTCATCTATTTGTGTGCTTCGCTGGGTCCCCAGCCACCATCTTTGAC  2589
Qy  1392  TTTTTCCGGGTGTCCTTCCTTGCCAAAAATGATCTCTGCTCCTCCGGGGTCACCACGTCCTAC  1451
Db  2590  AACTATGACCTACTGCTTGGCCTCCATGCGTTGGTTCTTCCAATGAGACCTTTGATGGG  2649
Qy  1452  ATCCTCGTTCTGGAGTCAGCGGATCAGCCAGGAC-----------------   1486
Db  2650  CTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAAATATATGACCCCGTGATTCTGCTG  2709
Qy  1487  --------TGGGGGTGGTGCGTCTCCGGGGG                            1538
Db  2710  GTGTTTGCGTGGCGTGATCGTGGAAGTGCTCAGCAGGTGGAGTCGACTGCGCCCGCCTAGAC  2769
Qy  1539  CTCTTCTCCTGTGCGCTGGCCCTGGCCCTGCGCCGTGGACATCGAGGCTGGAC  1598
Db  2770  TTCCTCCTGGAAACTACAGGCAACAGCGGGGAGGAGGAGGAGGAGGACTACAGGCATAC  2829
Qy  1599  TACCTCTGGGCCGCACAGGCAGAGGGAGGAGGACATGGAAGCTGGAC  1658
Db  2830  AACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTCCTGGCCCCGG  2889
Qy  1659  AACAGGCGCATCCTCCTTCAACCTGCCCCACGTCGGCCCACGCTTCCTCATGTCC  1718
Db  2890  GAGGCCGCGCAATGATGAACTCTACTATCAGTCGTCTGAGTGTGTGCGTCTGTATGTTTGCC  2949
Qy  1719  AACCCTCGGAACATGGACCTTCTACTACCAGTCCTACTCCCAGGTGGGCGTCATGTTTGCC  1778
Db  2950  TCCAATGCCAACTTCTCTGAGTGTCATGTGGAGCGGAGGCAAACAATGAGGGTGTCGAG  3009
Qy  1779  TCCATCCCAACTTCAATGACTTCTACATCGAGCTGGACGGCAACAACATGGGGGGTGGAG  1838
Db  3010  TGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGGAGGAGCGG  3069
Qy  1839  TGTCTGCGGCCTTCTCAACGAGATCATCGCCGACTTTGACGAGCTTGACGAGCTCATGGAAAAAGACTTT  1898
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Qy  1899  TACAAGGACATAGAAGAAGATCAAGACCATCGGGACGCCATTACATGCCGCGTGTGGGGCTA  1958
Db  3130  AACGCC---------AGCACCTACGATCAGGTGGCGGCCCTGGCT  3180
Qy  1959  GCGCCCACCTCGGGGACCAAGGCTAAGAAGTCCATCTCCTCCCACCTGAGCACGCTGGCCG  2018
Db  3181  GACTACGCCATGCGGCTCATGGAGCAGAGTGAAGCACATCAATGAGACACTCCTTCAACAAT  3240
Qy  2019  GACTTTGCCATTGAGATGTTTGACGTTCTGGATGAAATCAACTCAACCACCAGTCTTACAACGAC  2078
Db  3241  TTCCAGATGAAGAGATTGGGCTGAACATGGGCCCAGTCGTGTCAACATGGGGCTCGG  3300
Qy  2079  TTTGTCCTCCGAGTTGGCATCAATGTTGGCCCTGTGTGGTGGGAGTGATTGGCGTGGCTCGC  2138
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Qy  2199  GGGGTCCAGGGCCAGGGACTCAGGTGACTGAGGAAGTCCACCGGCGTCGAGAAGGTGCCCC  2258
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Qy  2259  TACCACTTTGTGTGCCGAGCCAAAGTCAGTGTCAGGTGCAAAGGCAGAGATGTTGACATAC  2318
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RESULT 14
US-09-925-297-352
; Sequence 352, Application US/0992597

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; Patent No. US20020081659A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA105
;  CURRENT APPLICATION NUMBER: US/09/925,297
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05989
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 928
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
;  LENGTH: 2601
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc feature
;  LOCATION: (2520)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc feature
;  LOCATION: (2572)
;  OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-352

Query Match             11.5%;  Score 408.2;  DB 9;  Length 2601;
Best Local Similarity   51.4%;  Pred. No. 2e-105;
Matches 1308;  Conservative    1;  Mismatches 1139;  Indels   97;  Gaps   12;
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Db     34 AACAGACCGCCAAGCACCCGCCAAGGCCTTCCTGGAGGCCCAGTCGCTGGAGGTGGAAGAT 93

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Db     94 GAACCTGGAAGAGCAGAGCCACCAGCAGCCACCTCATGTTTCCATCCTGCCCAAGCA 153

Qy   1047 CGTTGCCCATGGAGATGAAAGAAGACATCAACACA----------AAAAAGAAGACATGAT 1097
              |||| | |||||| |||  |||  |||
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Qy   1098 GTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCTCGTTTGCAGACATTGA 1157
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Db    214 GTTCAACACCATGTACCGTCACGATGACACATGTGTCAGACGTCAGCAGATCGT 273

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Db    274 GGGCTTTACCCAGGCTGTCTTCTGCCAGTGCCCAGGAGCTGGTTGTGAAGCTGCATCACGA 333

Qy   1218 GCTCTTTGCCCGGTTGACAAGCTGCTGCGCGGAGAATCACTGCTGGAGGATCAAGATCTT 1277
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Qy   1278 GGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCCCGGGGGCCCGACCATGCCCACTG 1337
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Db    454 CTCCATCCCATGGGGCCATGGGGAGCCGGCCATCCTCGTATGTGGCGGGAGAAGACCAA 513

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Qy   1518 GGCAGGAGGCCCGGGGCTTGGCCGGCATCCCATCCACATCACTCGGCAACACTGCAGTACCTGAACGG 1577
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Qy   1638 CATTGAGACTTTCCTCATCCTGGGCGCC-AGCCAGAAACGGAAAGGAGAGAGGCCATGC 1696
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Db   1101 TAGTAAAGAGAGAAACACCTTCCTCTTGTCCATGCGGTTCATGGGTTCATGGAGGTGAAGAT 1160

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; LENGTH: 463
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; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(463)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4198

Query Match             11.1%;    Score 394.2;   DB 11;    Length 463;
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Job time : 1444 secs
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc.
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;   TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;   FILE REFERENCE: 20411-756
;   CURRENT APPLICATION NUMBER: US/09/918,995
;   CURRENT FILING DATE: 2001-07-30
;   PRIOR APPLICATION NUMBER: US/09/235,076
;   PRIOR FILING DATE: 1999-01-20
;   NUMBER OF SEQ ID NOS: 38054
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4198
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           Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

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                                             7537.466 Million cell updates/sec

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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:      1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
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                               SUMMARIES
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    2  3484.8    98.1    3549  4  US-09-008-097-5            Sequence 5, Appli
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    5  2810.4    79.1    4131  3  US-08-726-214-11           Sequence 11, Appl
    6  1763.4    49.6    1812  4  US-09-008-097-3            Sequence 3, Appli
    7    1761    49.6    4523  4  US-09-473-716-1            Sequence 1, Appli
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    9   604.4    17.0    3978  3  US-08-726-214-1            Sequence 1, Appli
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   11   485.2    13.7    4601  3  US-08-726-214-15           Sequence 15, Appl
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   40    66.6    1.9    2013  4  US-09-205-426-176         Sequence 176, App
   41    66.6    1.9    2172  2  US-08-997-080-173         Sequence 173, App
   42    66.6    1.9    2172  2  US-08-997-362-173         Sequence 173, App
   43    66.6    1.9    2172  3  US-09-095-855-173         Sequence 173, App
   44    66.6    1.9    2172  4  US-09-324-542-173         Sequence 173, App
   45    66.6    1.9    2172  4  US-09-205-426-173         Sequence 173, App

                                ALIGNMENTS

RESULT 1
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
;  APPLICANT:  Tomlinson, James E.
;  APPLICANT:  COR Therapeutics, Inc.
;  TITLE OF INVENTION:  CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
;  TITLE OF INVENTION:  CYCLASE
;  FILE REFERENCE:  44481-5028-01-US
;  CURRENT APPLICATION NUMBER: US/09/474,076
;  CURRENT FILING DATE:  1999-12-12
;  PRIOR APPLICATION NUMBER:  PCT/US98/13694
;  PRIOR FILING DATE:  1998-07-01
;  PRIOR APPLICATION NUMBER:  60/070,904
;  PRIOR FILING DATE:  1997-07-01
;  PRIOR APPLICATION NUMBER:  08/886,550
;  PRIOR FILING DATE:  1997-07-01
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4942
;   TYPE: DNA
;   ORGANISM: human type VI adenylyl cyclase
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (145)..(3648)
US-09-474-076-1

  Query Match             99.8%;  Score 3545.6;  DB 4;  Length 4942;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3548;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 204

Qy         61 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GAACGCAATGGGCAGAAGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 264

Qy        121 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CCCCGCTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGCGGGCCCC 324

Qy        181 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 384

Qy        241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300
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us-09-750-240-10.rni

116

138

212

(handwritten annotations: Arg, Arg, Arg, His, Ser, Ser)

Db / Qy sequence alignment (DNA), residues 301–2604

1184

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Qy   3541 AAGTGGGGACT 3552
          ||||||||||||
Db   3685 AAGTGGGGATT 3696
```

```
RESULT 2
US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
GENERAL INFORMATION:
     APPLICANT: Hammond, H. Kirk
     APPLICANT: Insel, Paul A.
     APPLICANT: Ping, Peipei
     APPLICANT: Post, Steven R.
     APPLICANT: Gao, Meihua
     TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
     TITLE OF INVENTION: HEART FAILURE
     NUMBER OF SEQUENCES: 9
     CORRESPONDENCE ADDRESS:
         ADDRESSEE: MORRISON & FOERSTER
         STREET: 755 PAGE MILL ROAD
         CITY: PALO ALTO
         STATE: CA
         COUNTRY: USA
         ZIP: 94304-1018
     COMPUTER READABLE FORM:
         MEDIUM TYPE: Diskette
         COMPUTER: IBM Compatible
         OPERATING SYSTEM: DOS
         SOFTWARE: FastSEQ for Windows Version 2.0
     CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/09/008,097
         FILING DATE:
         CLASSIFICATION:
     PRIOR APPLICATION DATA:
         APPLICATION NUMBER:
         FILING DATE:
     ATTORNEY/AGENT INFORMATION:
         NAME: Dylan, Tyler M
         REGISTRATION NUMBER: 37,612
         REFERENCE/DOCKET NUMBER: 22000-20567.21
     TELECOMMUNICATION INFORMATION:
         TELEPHONE: 650-813-5600
         TELEFAX: 650-494-0792
         TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
     SEQUENCE CHARACTERISTICS:
         LENGTH: 3549 base pairs
         TYPE: nucleic acid
         STRANDEDNESS: single
         TOPOLOGY: linear
     FEATURE:
         NAME/KEY: Coding Sequence
         LOCATION: 1..3501
     OTHER INFORMATION:
US-09-008-097-5
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Query Match             98.1%;  Score 3484.8;  DB 4;  Length 3549;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
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Qy      1 ATGTCATGGTTTAGTGGGCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCATGGTTTAGTGGGCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT 60
```

```
Qy     61 GAACGCAATGGGCAGAAGCGGTTCGCGGGCCGGTTCGCGGGCCGGTTCGCACTCGCACG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAACGCAATGGGCAGAAGCGGTTCGCGGGCCGGTTCGCGGGCCGGTTCGCACTCGCACG 120
```

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Qy    121 CCCGGCTATATGAGCTGCCTCCCGGGATGCAGAGCCACCCAGCCCACCCCTGCGGGCCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGGCTATATGAGCTGCCTCCCGGGATGCAGAGCCACCCAGCCCACCCCTGCGGGCCCC 180
```

```
Qy   2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGACACATCAGCAGCATCGGGAAGTTGGCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2605 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC 2664
```

```
Qy   2521 ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCGCTGGGTCCCCAGCCACC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2665 ATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCGCTGCGTGGGTCCCCCAGCCACC 2724
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```
Qy   2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCTTGGCTTCTTCCAATGAGACC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2725 ATCTTTGACAACTATGACCTACTGCTTGGCGTCTTGGCTTCTTCCAATGAGACC 2784
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Qy   2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATGACCCCTGTG 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2785 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATGACCCCTGTG 2844
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Qy   2701 ATTCTGCTGTGTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTGCGACTGCC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2845 ATTCTGCTGTGTGTTGCGCTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTGCGACTGCC 2904
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```
Qy   2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGAGGACGATGGAGGAGCTA 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2905 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGAGGACGATGGAGGAGCTA 2964
```

```
Qy   2821 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2965 CAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 3024
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```
Qy   2881 CTGCCCCGGAGCGGCCGCAATGATGAACTCTACATATCGTGTGAGTGTGGCTGTT 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3025 CTGCCCCGGAGCGGCCGCAATGATGAACTCTACATATCGTGTGAGTGTGGCTGTT 3084
```

```
Qy   2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAAACAATGAG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3085 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCATGTGGAGCTGGAGGCAAACAATGAG 3144
```

```
Qy   3001 GGTGTCGAGTGCCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3145 GGTGTCGAGTGCCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3204
```

```
Qy   3061 GAGGAGCGCGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3205 GAGGAGCGCGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3264
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```
Qy   3121 TCAGGGCTGAACGCCAGCACCTACGATCCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3265 TCAGGGCTGAACGCCAGCACCTACGATCCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3324
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Qy   3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3325 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3384
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```
Qy   3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGCAGTGTCATCGGGGCTCGG 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3385 TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGCAGTGTCATCGGGGCTCGG 3444
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```
Qy   3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3445 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3504
```

```
Qy   3361 GGGGTCCCCGACCGAATCCAGGTGACCACGACCGTACCAGGTTCAGCTGCCTGCCAAGGGC 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3505 GGGGTCCCCGACCGAATCCAGGTGACCACGACCGTACCAGGTTCAGCTGCCTGCCAAGGGC 3564
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```
Qy   3421 TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGAGGGGACAAGGGGAGATGACCACCTAC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3565 TACCAGCTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGGGAGGGGACAAGGGGAGATGACCACCTAC 3624
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Qy   3481 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3625 TTCCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC 3684
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Nucleotide sequence alignment (Qy = query, Db = database)

Left column:

```
Qy   181 CCTCGGTGCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCTCGGTGCCCTGGCAGGATGACGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240

Qy   241 GAGCTGGGGCAGTGCGGGCAGTGCCTGGCCTTCGGGCTTCGAGGATACCGAGTGACAACGACAGCG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAGCTGGGGCAGGCTGAGGTGGCGGGCAGTGCCTGGCCTTCGGGCTTCGAGGATACCGAGTGACAACGACAGCG 300

Qy   301 GGCGGACGCGGCTGAGGTGGCCGCCCCGACGCCGTGCCGCCGGAGTGGGCGCGGCGATCCTGCTGGCGC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGCGGGACGGCGCTGAGGTGGCTGAGGTGGCCCCGACGCCGTGCCGCCGGAGTGGGCGCGGCGATCCTGCTGGCGC 360

Qy   361 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGTCGGAGCGCCTGTAC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGTTTGGTGCAGGTGTTCCAGTGCAGGTGTTCCAGTCGGAGCGCCTGTAC 420

Qy   421 CAGCCGTACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGCTCAGCCTGCCTAT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAGCCGGTACTTTTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGCTCAGCCTGCCTAT 540

Qy   481 CTGCTCACAGGGGTGCTGCTTCCACGCCTGTCGTGGGGCTCATGGTGGTTGTAACCGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CTGCTCACAGCGGTGCTGCTTCCACGCCTGTCGTGGGGCTCATGGTGGTTGTAACCGG 600

Qy   541 GTGGCACTGTTGGCCTGGCCGCGCCTGTTCGTGTGGGGCTCATGGTGGTTGTAACCGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTGGCACTGTTGGCCTGGCCGCGCCTGTTCGTGTGGGGCTCATGGTGGTTGTAACCGG 600

Qy   601 CATAGTTCCCGCCAGGACTCCATGTGGTGGTTACGTTGGTGCTGTGGGCATCCTGGGCG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CATAGTTCCCGCCAGGACTCCATGTGGTGGTTACGTTGGTGCTGTGGGCATCCTGGGCG 660

Qy   661 GCAGTGCAGGTCGGGGAGCGCTCTCGCAGCAGACCCCGCCAGCCCCTCGGCGGGCCTCTGG 720
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   661 GCAGTGCAGGTCGGGGCGGCGCTTCGCAGCAGACCCCGCCAGCCCCTCGGCGGGCCTCTGG 720

Qy   721 TGCCCTGTGTTCTTTGTGCTACATCGCCTACACGCCTCCTCCCCATCCGCGGCATGCGGCTGCC 780
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   721 GTCCCCTGTGTTCTTTGTCTTTGTACATCCGCGGCCTCCTCCCCATACGGCGGCATGCGGCTGCC 780

Qy   781 GTCCTCAGCGGCCTGGGCCTCTCCCACCTTGATCTTTGGCCTGGCAACTTAACCGT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTCTTCAGCGGCCTGGGCCTCTCCCACCTTGATCTTTGGCCTGGCAACTTAACCGT 840

Qy   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTTGCCAATGTGCTGCTGTTCCTCTGCACCAAC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGTGATGCCTTCCTCTGGAAGCAGCTCGGTTGCCAATGTGCTGCTGTTCCTCTGCACCAAC 900

Qy   901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGGCCTTTCAGGAG 960
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GTCATTAGCATCTGCACATCTGCACATCCAGCAGAGGTGTCTCAGCGGCCTTTCAGGAG 960

Qy   961 ACCCGGCGGTTACATCCAGGGCCTGCTTCACCTGCGGTGGCAGCAGCAGCAGGAGCGCG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCCGGCGGTTACATCCAGGGCCTGCTTCACCTGCGGTGGCAGCAGCAGCAGGAGCGCG 1020

Qy  1021 CTGGCTGCTGCCTTCCTCTGGAAGCAGCTCGGTTATTGCCGTAATGCTGCCAATGTTGCCACGTTGTCTCAGAGGTGTCTCAGGAG 1080
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  1021 CTGGCTGCTGCCTTCCTCTGGAAGCAGCTCGGTTATTGCCGTAATGCTGCCAATGTTGCCACGTTGTCTCAGAGGTGTCTCAGGAG 1080

Qy  1081 AAAAAGAAGACATGATGTTCCACACAGTTCCACACAGTTGAAAGAAGACATGAAAGAGACATCAACACA 1140
         |||||||||||     |||||||||||||||||||||||||||||||||||||
Db  1081 AAAAAGAAGAC---ATGTTCCACACAGTTGAAAGAAGACATGAAAGAGACATCAACACA 1137

Qy  1141 CTGTTTGCAGACATTGAGGGGCTTCACCGGCTTCACCGGCTTCGACTGCGCTGCCAGGAGCTG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1138 CTGTTTTGCAGACATTGAGGGGCTTCACCGGCATCTTGCCATCTTGGCATCTGCGACTGCGCCAGGAGCTG 1197

Qy  1201 GTCATGACCCTGAATGAGTCCTTTGACAAGTCTGGCTTGCGGAGAATCACTGC 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1198 GTCATGACCCTGAATGAGTCCTTTGACAAGTCTGGCTTGCGGAGAATCACTGC 1257

Qy  1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCCGAGGGCCCGG 1320
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Right column:

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGGCCGG 1317

Qy  1321 GCCGACCATGCCCACTGTCGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCCGCTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1318 GCCGACCATGCCCACTGTCGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCCGCTG 1377

Qy  1381 GTACGTGAGGTGACAGGTGTGAACATGCGCGTGGGCATCCAGCGGGCGCGTG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378 GTACGTGAGGTGACAGGTGTGAACATGCGCGTGGGCATCCAGCGGGCGCGTG 1437

Qy  1441 CACTGCGGCGTCCTTGCTTCGCGAAATGCAGTTCGATGTGTGGTTCCAATGATGTGACC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1438 CACTGCGGCGTCCTTGCTTCGCGAAATGCAGTTCGATGTGTGGTTCCAATGATGTGACC 1497

Qy  1501 CTGGCCAACCACCATGGAGGCAGGAGCCGGTGGCCGGGCCATCCAATCACTCGGGCAACA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1498 CTGGCCAACCACCATGGAGGCAGGAGCCGGTGGCCGGGCCATCCAATCACTCGGGCAACA 1557

Qy  1561 CTGCAGTACCTGAACGGGGACTACGAGGTGAGCCGGTGGCTGCGACGCACGCG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1558 CTGCAGTACCTGAACGGGGACTACGAGGTGAGCCGGTGGCTGCGACGCACGCG 1617

Qy  1621 TACCTCAAGGAGCAGCAGCACATTGAGACTTCCTCATCCTGGGCGCGCCAGAAAACGAAA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1618 TACCTCAAGGAGCAGCAGCACATTGAGACTTCCTCATCCTGGGCGCGCCAGAAAACGAAA 1677

Qy  1681 GAGGAGAAGGCCATGCTGGGCCAAGCTCGGGCGACTCGGGCCAACTCCATGGAAGGGCTG 1740
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Db  1678 GAGGAGAAAGGCCATGCTGGGCCAAGCTCGGGCGACTCGGGCCAACTCCATGGAAGGGCTG 1737

Qy  1741 ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1738 ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGC 1797

Qy  1801 CAGATGGCATTGATGATTCCAGCAAAGACAACACGGGGCACCCAAGATGCCCTGAACCCT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1798 CAGATGGCATTGATGATTCCAGCAAAGACAACACGGGGCACCCAAGATGCCCTGAACCCT 1857

Qy  1861 GAGGATGAGGTGGATGAGTTCCTGCCGCGTGCATCGATGCCGCAGCATTGATCAGCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1858 GAGGATGAGGTGGATGAGTTCCTGCCGCGTGCATCGATGATCGATGCCGCAGCATTGATCAGCTG 1917

Qy  1921 CGGAAGGACCATGTGCGCCGGTTTCGTGCTCACCTTCCAGAGAGGAGGATCTTGAGAAGAAG 1980
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  1918 CGGAAGGACCATGTGCGCCGGTGTTTTCGTGCTCACCTTCCAGAGAGGAGGATTTGAGAAGAAG 1977

Qy  1981 TACTCCCGGAAGGTGGATCCCCGGCTTCGGAGCCTGAGTGCTGCCCTGGTGCCCTGTCTTC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1978 TACTCCCGGAAGGTGGATCCCCGGCTTCGGAGCCTGAGTGCTGCCCTGGTGCCTGGTCTTC 2037

Qy  2041 TGCTTCATCTCGCTTCATCTGCTTCCTGCTCTAATCACCGGTGCTAATCACCGGTGCTTGGGATC 2100
         |||||||||||||||||||||||||||||||||||||||| || |||||||||||||||||
Db  2038 TGCTTCATCTCGCTTCATCTGCTTCCTGCTCTAATTTCCCACGTGCTAATCACCGGTGCTTGGGATT 2097

Qy  2101 TATGCCAGCATCTTCCTGCTTCCCTAAGGCCCGCAACGTGCTGTCAATCACCGTGCTGTCTGCCAACG 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2098 TATGCCAGCATCTTCCTGCTTCCCTAAGGCCCGCAACGTGCTGTCAATCACCGTGCTGTCTGCCAACG 2157

Qy  2161 GGTTCTCGTTCCCTGCTCTGTTCCCTGCTCTGTTTACTTCTGCCATTGCCAAC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2158 GGTTCTCGTTCCCTGCTCTGTTCCCTGCTCTGTTTACTTCTGCCATTGCCAAC 2217

Qy  2221 CATAGACACCGAGTTGGCATCTTTTCCGCTCGTCGTTGTTTACTTCGCCAGGAGCTGTTGCAGCGGCTG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2218 CATAGCCACCGAGTTGGCATCTTTTCCGCTCGTCGTTGTTTACTTCGCCAGGAGCTGTTGCAGCGGCTG 2277

Qy  2281 ATGTTCACCTGTAACCACACACCCCATACGGAGCGTGCAGCGCGGATGCTGAATTTAACA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2278 ATGTTCACCTGTAACCACACACCCCATACGGAGCGTGCAGCGCGGATGCTGAATTTAACA 2337

Qy  2341 CCTGCTGACATCACTGCCTGCCACCTGCAATTACTCCTGGGCCTCAATTACTCCTCTGGCGATGCT 2400
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Db   2338  CCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCCTGGATGCT  2397
           ||||||||||  ||   ||| ||||| |||| ||| || |  |   ||||||||||||||
Qy   2401  CCCCTGTGTGAGGGACCATGCCCACCTGCAGCTTCCTGAGTACTTCATCGGGAACATG  2460
Db   2398  CCCCTGTGTGAGGGACCACCATGCCCACCTGCAGCTTCCTGAGTGTCCATCGGGAACATG  2457

Qy   2461  CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
           ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   2458  CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2517

Qy   2521  ATGATCTTTGTCTTGGGGCTCATCTATTGGTGGTCTTCTGCTTCCCGGTCCCCCAGCCACC  2580
           ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   2518  ATGATCTTTGTCTTGGGGCTCATCTATTGGTGGTCTTCTGCTTCCCGGTCCCCCAGCCGCC  2577

Qy   2581  ATCTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2578  ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC  2637

Qy   2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGTGGCCCTCAAATATATGACCCCCTGTG  2700
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Db   2638  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGTGGCCCTCAAATATATGACCCCCTGTG  2697

Qy   2701  ATTCTGCTGTGTGTTCGCGCTGGCCGCTGTATCTGACATGCTCAGCAGGTGGAGTGACTGCC  2760
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Db   2698  ATTCTGCTGTGTGTTCGCGCTGGCCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCC  2757

Qy   2761  CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGAAGGAGGAGATGGGAGGAGCTA  2820
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2758  CGCCTAAACTTCCTCTGGAAACTACAGGCAACAGGGAGAAAAAGAGGAGATGGGAGGAGCTA  2817

Qy   2821  CAGGCATACAACCGGAGCGTGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2818  CAGGCATACAACCGGAGCGTGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC  2877

Qy   2881  CTGGCCCGGGAGCGGCGCCGCAATGATGAAGTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2878  CTGGCCCGGGAGCGGCGCCGCAATGATGAAGTCTACTATCAGTCGTGTGAGTGTGTGGCTGTT  2937

Qy   2941  ATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  3000
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Db   2938  ATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG  2997

Qy   3001  GGTGTCGAGTGCTGCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC  3060
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Db   2998  GGTGTCCGAGTGCTGCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC  3057

Qy   3061  GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
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Db   3058  GAGGAGCGGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3117

Qy   3121  TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3180
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Db   3118  TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT  3177

Qy   3181  GACTACGCCATGCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3178  GACTACGCCATGCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT  3237

Qy   3241  TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGTGTCATCGGGGCTCGG  3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3238  TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGTGTCATCGGGGCTCCG  3297

Qy   3301  AAGCCACAGTATGCAGATTGGGCTGGGGAAACAGTGAAATGTCCTAGTCGTATGGACAGCACG  3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3298  AAGCCACAGTATGCAGATTGGGCTGGGGAAACAGTGAAATGTCTCTAGTCGTATGGACAGCACG  3357

Qy   3361  GGGGTCCCCGACCGGAATCCAGTTGACCACGACAGTTCTACCAGGTTCAGCTGCCAAGGGC  3420
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Db   3358  GGGGTCCCCGACCGGAATCCAGTTGACCACGACAGTTCTACCAGGTTCAGCTGCCAAGGGC  3417

Qy   3421  TACCAGCTTGGAGTTGTCGAGGGGTGGTCAAGGTGAAGGGGAGCAAGATGACCACCTTAC  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3418  TACCAGCTGGAGTTGTCGAGGGGTGGTCAAGGTGAAGGGGAGCAAGATGACCACCTTAC  3477
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Db   3481  TTCCTCAATGGGGGCCCCCAGCAGTAACAGGGCCCCAGCCACAAATTCAGCTGAAGGGACC  3540
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Db   3478  TTCCTCAATGGGGGCCCCCAGCAGTAACAGGGCCCAGCCACAAATTCAGCTGAAGGGACC  3537

Qy   3541  AAGGTGGGCACT  3552
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Db   3538  AAGGTGGGCCACT  3549
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RESULT 3
US-07-793-961A-1
; Sequence 1, Application US/07793961A
; Patent No. 5334521
GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; ADDRESSEE: American Cyanamid Company
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1

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Query Match            85.9%;  Score 3051.2;  DB 1;  Length 4046;
Best Local Similarity  91.8%;  Pred. No. 0;
Matches 3260;  Conservative   0;  Mismatches 283;  Indels  9;  Gaps  3;

Qy     1  ATGTTCATGGTTTAGTGGGCTCCTGGTCCTAAAGTGGGATGAACGGAAAACAGCCTGGGGGT  60
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Db   131  ATGTCGTGGTTTAGTGGGCTTCCTGGTCCTGTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT  190

Qy    61  GAACGCAATGGGCCAGAAGGGTTCGCGGGCCGTGGCCATGGGCCACTCGGCGGTGGCTTCGCACG  120
          ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db   191  GAACGCAATGGGCAGGAGGAGCGGT---CCACGGCCGCGGGACTCCGGACCCAGGCCAGTGGCTTCTGCACG  247

Qy   121  CCCCGCTATATGAGCTGCCTCCGGGATGCTGCCTCCGGGATGCTGAGAGCCACCCAGCCCCAGCCCCCGCGGCCCCC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248  CCCCGCTATATGAGCTGCCTCCGGGATGCGGATGCGGAGAGCGGCAGCCCCCAGTCCCCAGTCCCCGCGGCTCCC  307
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Qy  181 CCTCGGTGCCCCTGGCAGGATGACGCGCCTTCATCCGGAGGGGCGGCCCAGGCAAGGGCAAG 240
        |||||||||||||||||||||||| |||| |||||||||||||| ||||||||| ||||||||
Db  308 CCTCGGTGCCCCTGGCAGGATGAGGAGGCCTTCATCCGGAGAGGCGGCCCGGGCAAGGGCACG 367

Qy  241 GAGCTGGGGCTGCGGGCAGTGCCCTGGGCTTCGAGGTGACAACGACAGCG 300
        ||||| |||||| ||||| |||||||||| |||||||     ||||||||
Db  368 GAGCTGGGGCGGCGGGCGGTGCCCTGGGCCTTCGAGCACTGAG---CCATGTCAGCG 424

Qy  301 GGCGGACGGCTGAGGTGGCGCCCGAGACGCGGCCCCAGGAGTGGGCGGATCCTGCTGGCGC 360
        |||||||||  ||||| || ||||||||| ||  || ||||| |||||||||||||| |||
Db  425 GTTGGGGACCAGCTGGAGGTGGGCCCGAGCGTGACCCCGGGAGTAGGCGGATCCTGCTGGCGC 484

Qy  361 CGTCTGTGCAGGTGTTCCAGTCGAAGCAGTTCGGCCAAGCTGGAGCGCCCTGTAC 420
        |||||||| ||||||| |||||||||||||| |||||||||||||||||||||||||
Db  485 CGTCTGTGCCCCAGGTGTTCCGCTCGAAGCAGTTCGGCCAAGCTGGAGCGCCCTGTAC 544

Qy  421 CAGGCGGTACTTCTTCAGATGAACCAGAGACAGCCTGACGCTGCTGATGGGCGGTGGTG 480
        |||||||||||| || ||| |||||| |||||||| || ||||| ||||||||||||||
Db  545 CAGGCGGTACTTCTTTCAGATGAACCAGCACCAGCCTCCATGCTGCTGATGGGCGGTGGTG 604

Qy  481 CTGCTCCACAGCGGTGCTGCTGCTTCCACCGCCGCACCCCGCCCTCAGCCTGCCTAT 540
        ||| ||||| |||| ||||||||||| |||||||||||||||||||||||||||||||
Db  605 CTGCTGACAGCGGTGCTGCTAGCCTTCCATGCTGCCACCCCGCCCTCAGCCTGCCTAC 664

Qy  541 GTGGCACTGTTGGCCTGCCGCCCGTGTCGTGGGGCTCATGGTGTGTAACCGG 600
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Db  665 GTGGCCCTGCTGGCCTGCCGCCCGTGCTCGTGGCGCTCATGGTGTGTAACCGG 724

Qy  601 CATAGTTCCGCCAGACTCCATGTGGTGAGTTACGTGGTGTGGCATCCTGGCG 660
        || |||||| ||||||||||||||| ||||| |||||||||| ||||||||||
Db  725 CACAGCTTTCGCCAGGACTCCATGTGGTGAGTTGAGCGTGGTGTGGCATCCTGGCA 784

Qy  661 GCAGTGCAGGTCGGGGGCGCTCCGCCAGCACCCGCGCAGCCCCTCTGG 720
        || || |||||| |||| ||||||||| |||| || || |||||||||
Db  785 GCCGTTCAGGTTGGGGGTGCCCTCTGGAGCCAACATGCTCGGTGCTGCCGGTGCCACCAAC 844

Qy  721 TGCCCTGTGTTCTTTGTCTACATGCGCCTCTCCCATCCGCATCGGGGCTGCC 780
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Db  845 TGCCCTGTGTTTTTGTCTACATCCGCCTCTCCCATCCGCATCGCGGGGCAGCT 904

Qy  781 GTCCTTCAGCGCGCCTCGGCCCTGTCCAGCGCCCTGCATTGATCTTGGCTGGCAACTTAACCGT 840
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Db  905 GTCTTCAGTGGCCTCGGCCCTGTCCAGCGCCCTGCATTGATCTTGGCCTGGCAACTCAACCGC 964

Qy  841 GGTGATGGCCTTCCTCTGGAAGCAGCTCGGTGCCCATGGCCGGTGCGTGTCCTCTGCACCAAC 900
        || ||||||||||||||||||||| |||||||| |||| ||||||| ||||||||||||||||
Db  965 GGTGACGGCCTTCCTCTGGAAGCAGCTCGGTGCCCATGTGCCAGCAGTGCGTGCTCTGCACCAAC 1024

Qy  901 GTCATTGGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGGCCTTTCAGGAG 960
        ||||||||||||||||||| || |||||||| |||||||||| ||||||||||||
Db 1025 GTCATTGGCATCTGCACACACTGCCAGCCGCTGAGGTCTCTCAGCGGCCTTTCAGGAG 1084

Qy  961 ACCCGGCGGTTACATCCAGGGCCCCGGCTTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
        || |||| |||||||||||| ||||||||||||||||||||||| || |||| ||||||||||
Db 1085 ACCCGGCGGTTACATTCAGGGCCCCGGCTTCCACCTGCAGCATGAGAACCGGCAGCAGGAGCGG 1144

Qy 1021 CTGCTCTGTCGCGTATTGGCCCCCAGCGTTGCCCATGGAGATGAAAAAGACATCAACACA 1080
        || || |||||| ||||||||||||||| ||||||||||||| |||||| |||||| |||
Db 1145 CTGCTGCTGTCGCCGTGTTGGCCCCCAGCGTTGCCCATGGAGATGAAAAAGAAGATATCAACACA 1204

Qy 1081 AAAAAGAGACACATGATGTTCCACATAGTCCACAGATCTACATACAGAGACATGACAATGTCAGCATC 1140
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Db 1205 AAGAAGAGACATGATGTTCCACATCAGTCCACAGATCTACATACAGAGACATGACAATGTCAGCATC 1264

Qy 1141 CTGTTTGCAGCATTGAGGGGTTCACCTGCCCGGCTTCACCTGCCACTGCCAGGAGCTG 1200
        || ||||||| |||||||| |||||||||||||| ||||||||||| ||||||||||||
Db 1265 CTGTTTGCGCAGCATTGAAGGCTTCACCTGCCCGGCTTCACCTCCACCGCCAGGAGCTG 1324

Qy 1201 GTCATGATCGCTCGAATGCTGCTTGCCCTCGGGTTTGACAAGCTGGCTCGCGGGAATCACTGC 1260
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Db 1325 GTCATGATCGCTCTGAACGACCCTGGGTTTGACAAGCTGGCTCGTGCGGAAAATCACTGC 1384

Qy 1261 CTGCTGACATCAAGAGATCTTTGGGGGGACTGTTACTCTGTGTCAGGGGCTGCCCGAGGCCCCGG 1320
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(Db in right column)
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Right column:

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Db 1385 CTGAGGATCAAGATCTTTAGGGGACTGTTACTCTGTGTGTCGGGGCTGCCCGAGGCCCCGG 1444

Qy 1321 GCCGACCATGCCCACTGCTGTGTGTGGAGATGGGGTAGACATGGATGAGGCCATCTCGCTG 1380
        || |||||||||||||||||| ||||| |||||| |||| ||||| |||||||||||||||
Db 1445 GCAGACCATGCCCACTGGTGTGTGTGGAGATGGGGTGGACATGGATGAGGCCATCTCGCTG 1504

Qy 1381 GTACGTGAGGTGACAGGTGTGAAATGTGAACATGCGGCGTGGCATCCACAGCGGGCGCGGTG 1440
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Db 1505 GTGCGTGAGGTGGACAGGTGTGAACGTGAACATCCGGCGTGGGCATCCAGCAGCGGGCGGTG 1564

Qy 1441 CACTGCGGTGCCTTGCCTTCGGCGAAATGAAGGTTGCGCCAAGCTGGTGGTCCAATGATGTGACC 1500
        ||||| ||||||| ||||||||||||||||| ||||| | |||||||||||| |||||||||||
Db 1565 CACTGTGGTGCCTTGCCTTCGGCCTCGCCGGGAAATGCAGTTGCACGTGTGGTCCAATGACGTGACT 1624

Qy 1501 CTGGCCAACCACATGGAGGCAGGAGGCCGGCTGGCCGCATCCACTCACTCCGGCAACA 1560
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Db 1625 CTGGCCAACCATATGGAGGCC---GGCCCGGCCGCCGCATCCACACCCGGCCACG 1681

Qy 1561 CTGCAGTACCTGAACCGGGAGACTACGAGGTGGAGCCTTCTCCCATCTGGTGCGGCAAGCGCG 1620
        |||||||||||||||||| || ||||||||||||||||||||||| || ||||||||||| ||
Db 1682 CTGCAGTACCTGAACCGGGAGACTACGAGGTGGAGCCTTCCTCCCATCTCCGGACCAAGCAACCG 1741

Qy 1621 TACCTCAAGGAGCAGCACATTGAGACTTGCGGCCAAGCTGGCCAGAAACGGAAA 1680
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Db 1742 TACCTCAAGGAGCAGCAGCACATCGAGACCTTCTCCGGAGCCAGCAAGAACGGAAA 1801

Qy 1681 GAGGAGAAGGCCATGCTGGGCCAAGCTCGAGCCGCTGCCAACTCATGGAAGGGCTG 1740
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Db 1802 GAGGAGAAGGCCATGCGTGGGCCAAGCTCGTGGCCGCGGCCAACTCCATGGAAGGCCTG 1861

Qy 1741 ATGCCGGCTGGGTTCCTGCTGTCCCGATCGTGCTCACCTTCCCAGGCCTTCCGC 1800
        || || |||| ||||||| |||| ||||| ||||||||||||||||||||||||
Db 1862 ATGCCACGCTGGGTGGCCGCGCCGCCTTCCTCGCCACGCTTCCCAGGCTTTTCGC 1921

Qy 1801 CAGATGGCATTGATGATTCAGCAAAGAACAACCGGGGCACCCAAGATGCCTGAACCCT 1860
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Db 1922 CAGATGGGCATTGATGATTCAGCAAAGAACAACCGGGGTGCCCAAGTGCCTGAACCCCC 1981

Qy 1861 GAGGAGAAGGCCATGGTGGATGAGTTCCTGCCGTGCATGATGCCCAGCATTGATCAGCTG 1920
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Db 1982 GAGGAGAAGGCCATGCGTGGATGAGTTCCTGCGTGCATGATGCCCAGCATCGATCAGCTA 2041

Qy 1921 CGGAAGGACCATGTGCGCCGGTTCTGCTCACCTTCGAGAAGAAG 1980
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Db 2042 CGGGAAGGACCATGTCCGCCGGTTCTGCTCACCTTCAGAGAGAAGAAG 2101

Qy 1981 TACTCCCGGAAGGTGATCCCCGGTTCAGGCCTTTCAGGAGGTTCTTTC 2040
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Db 2102 TACTCAAGGAAGGTGACCCCGCTCTTTCCCGGCCTGTTGCGCGTGTTTTTC 2161

Qy 2041 TGCTTCATCTGCTTCATCCTGCTTGGGCTGGCAACTTAACCGTGTGGGATC 2100
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Db 2162 TGCTTCATCTGCTTTATCCTGCTGTTCTTGCTTCCAACCTCCAACCGGTGGGGATC 2221

Qy 2101 TATGGCCAGCATCTTCCTGCTGCTGTAATCACCGTGTGCTGTCTGTGTACTCCTGT 2160
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Db 2222 TACGGCCAGTATCTTTGTGCTGTGCTGCTGATCACCGTGTGACCTGTCTGTACTCCTGT 2281

Qy 2161 GGTTCTTCTGTTCTCCTAAGGGCCCCAAGGCATGTTCCGCTCACGGCCA 2220
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Db 2282 GGCTCTCTTCTCTTCCCCAAGGGCTCTGCGACGTCTTTCCCGCTCTCGGGCA 2341

Qy 2221 CATAGACACCGAGTTGGCATCTTTTCGCTCGTTGTTACTTCTGCCAAC 2280
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Db 2342 CACAGACACTGTGGTTGGCATTTTTTCAGTCGTTGCTAGTGTTCACCTCGCCAAC 2401

Qy 2281 ATGTTCACCTGTAACACACCCCATACGGAGCTGTGCAGCCGATGCTGAATTTAACA 2340
        ||| |||||| ||| ||| ||||||||| ||||| |||||| |||||||||| ||||
Db 2402 ATGTTCACCTGTAACACACCACACCCCATCCGGGACCGTGTCAGCCGGATGCTGAATGTAACA 2461

Qy 2341 CCTGCTGACATCACTGCTGCCACCTGACACTGTTACTACTCTCTGCGGATGCT 2400
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Db   2462  CCCGCTGACATCACTGCCTGCGAGCAGCTCAATTACTCCTCTGGGCCTGGATGCT  2521

Qy   2401  CCCCTGTGTGAGGGCACCATGCCCACCTGCCAGCTTCCTGAGTACTTCATCGGCAGAACATG  2460
           || ||||||||||||| |||||||| |||| |||||||||| ||||| |||||| ||||||||
Db   2522  CGGCTGTGTGAGGGCACCGCACCCACTTGCAGCTTCCCTGAGTACTTCGTTGGGAACATG  2581

Qy   2461  CTGCTGAGTCTCTTGGCCAGCTCGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCC  2520
           ||||||| || ||| ||||| |||||||||||||||||||||||||||||||||||||||
Db   2582  CTGCTGAGTCTCTTGGCCAGCTCGTCTTTTCCTGCACATCAGTAGCATCGGGAAGTTGGCC  2641

Qy   2521  ATGATCTTTGTCTTGGGGCTCATCATCTATTGGTGCTGCTCGCTGGGTCCCCCAGCCACC  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   2642  ATGATCTTTGTCTTGGGGGTCATTTATTTGGTGCTGCTTCGCTGGGGCCCCCCAGCACC  2701

Qy   2581  ATCTTTGACAACTATGACCTACTGCTTGCGTCCATGGCGTTGGCTTCTTCCAATGAGACC  2640
           |||||| ||||||||||||||| |||||| ||||||||||||||||| ||||||||||||
Db   2702  ATCTTTGACAACTATGACCTGCTGCTTGCGTGTCCATGGCGTTGGCTTCTTCCAATGACACC  2761

Qy   2641  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTG  2700
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Db   2762  TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCACTGAAATACATGACCCCTGTG  2821

Qy   2701  ATTCTGCTGGTGTTGCGCGTGGGCCGCTGTATCTGCAGTCGTCAGCAGGTGGAGTCGACTGCC  2760
           ||||||||||| |||||||||||| ||||| ||| || |||| |||||||||||||| ||
Db   2822  ATTCTGCTGGTGTTTGCCCTGGGCCGCTGTATCTGCACGCGCCCAGCCAGGTGGAATCAACTGCA  2881

Qy   2761  CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGACGGATGGAGGAGCTA  2820
           || || |||||||||||||||||||||| || |||||||||||||||||||||||||||||
Db   2882  CGTCTGGACTTCCTCTGGAAACTGCAGGCAACAGCGGGGAGGAGGAGATGGAGGAGAGCTC  2941

Qy   2821  CAGGCATACAACCGGAGAGCGCTGCATAACATTCTGCCCAAGGACGTGCGGCCCCACTTC  2880
           ||||||| ||||| |||||||||||| ||||||||||| ||||||||||||||||||||||
Db   2942  CAGGCCTACAACCGAAGGCTGCTGCATAACATTCTGCCTAAGGACGTGCTGCTGCCCACTTC  3001

Qy   2881  CTGGCCCGGAGCGCGCCGCAATGATGAACTTCTACTATCAGTCGTGTGAGTGTGGCTGTT  2940
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Db   3002  CTGGCCCGGAGCGCGCCGCGAACGATGAGCTTCTACCAGTCGTGTGAGTGTGGCCCGTC  3061

Qy   2941  ATGTTGCTCCATTGCCAACTTCTCTGAGTTCTTATGTGGAGCTGGAGCGCAAACAATGAG  3000
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Db   3062  ATGTTTGCCTCCATTGCCAACTTTTCTGAGTTTCTTATGTGGAGCTGGAGGCAAACAATGAG  3121

Qy   3001  GGTGTCGAGTGCCTGCGGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC  3060
           ||||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   3122  GGTGTCGAGTGCCTGCGGCGGCTGCTCAACGAGATCATCGCCGACTTTGATGAGATCATCAGC  3181

Qy   3061  GAGGAGCCGGTTCCGGCAGCTGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC  3120
           |||||||||||||||| |||||||| ||||||||||||||| |||| ||||||||||||||||
Db   3182  GAGGAGCCGGTTCCGGCAGCTGCAGCTGGAGAAAATCAAGACGATCGGTAGCACCTACATGGCTGCG  3241

Qy   3121  TCAGGGCTGAACGGCCAGCACCTACGATCCAGGTGGGCCGCTCCCACACTGCCCCTGCT  3180
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Db   3242  TCGGGGCTGAACGGCCAGCACCTACGATCCAGGTGGGCCGCTCCCACACTGCCCTGCC  3301

Qy   3181  GACTACGCCATGCGGCTCATGGAGCAGGCTCAGAGCAAGAGCACATCAATGAGCACTCCTTCAACAAT  3240
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Db   3302  GACTATGCCATGCGGCTCATGGAGCAGGCTCAGAGCAAGAGCAGATCAACAATGAGCACTCCTTCAACAC  3361
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RESULT 4

US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
;   APPLICANT: Ishikawa, Yoshihiro
;   TITLE OF INVENTION: Cloning and Characterization of a
;   TITLE OF INVENTION: Cardiac Adenylyl Cyclase
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: American Cyanamid Company
;   STREET: One Cyanamid Plaza
;   CITY: Wayne
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07470-8426
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/240,357
;   FILING DATE: 10-MAY-1994
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gordon, Alan M.
;   REGISTRATION NUMBER: 30,637
;   REFERENCE/DOCKET NUMBER: 31,705-01
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-831-3244
;   TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4046 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 131..3625
US-08-240-357-1

Query Match   85.9%;   Score 3051.2;   DB 1;   Length 4046;
Best Local Similarity   91.8%;
Matches 3260;   Conservative   0;   Mismatches 283;   Indels 9;   Gaps 3;

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Qy     1  ATGTCATGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGT  60
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Db   131  ATGTCGTGGTTTAGTGGCCTCCTGGTCCCCAAAGTGGATGAACGGAAGACAGCCTGGGGT  190

Qy    61  GAACGCAATGGGCAGAAGGGTTCGCGCGGCCGTGGCACTCGGCGTTCTGCACG  120
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Db   191  GAACGCAATGGGCAGAAGGCGT---CCACGCGCGGCACTCGGACCAGTGCCTTCTGCACG  247

Qy   121  CCCGGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCACCTGCGGGCCCCC  180
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Db   248  CCCGGCTATATGAGCTGCTCCGGGATGCGGATGCCAGCAGCCCAGTCCCACCCCCTCCC  307

Qy   181  CCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGGCAGGATGACCACCTAC  240
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Db   308  CCTCGGTGCCCCTGCCCGCAGGATGAGGCCTTCATCCGGCAGGATGACCACCTAC  367
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Qy  1321  GCCGACCATGCCCACTCGTCTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG  1380
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Db  1445  GCAGACCATGCCCACTGGTGTGTGGAGATGGGGTGGGTGATCGAGGCCATCTCGCTG    1504

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Db  1505  GTGCGTGAGGTGACAGGTGTGAACGTGAACATCCGCGTGGGCATCCACAGCGGCGGCGTGTG  1564

Qy  1441  CACTGCGGCGTCCTTGGCTTCGTGGCGGAAATGCCAGTTGAGTGTGGTCCAATGATGTGACC  1500
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Db  1565  CACTGTGGTGTCCTGGCCTGCGGAAATGCCGACGTGGTGGTCCAATGACGTGACT  1624

Qy  1501  CTGGCCAACCACATGGAGGCAGGAGGCCGGGCCGCCGTCGGGCAACA            1560
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Db  1625  CTGGCCAACCATCCGGGGCC----GGCCCGGGCCGCCGGGCCACCGGGGCCACG    1681

Qy  1561  CTGCAGTACCTGAACCGGGACTACGAGGTGAGCCAGGCCGTGGTGCGAGCGCAACGCG  1620
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Db  1682  CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCCGCGGGTGGCGAGCCGGAACCG  1741

Qy  1621  TACCTCAAGGAGCAGCACATTGAGACTTCCATCATCCTCCTGGCGCGCCAGAAACGGAAA  1680
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Db  1742  TACCTCAAGGAGCAGCAGCATCGAGACCTTCCTCATCCTGGAGCCAGCCAGAAACCGGAAA  1801

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Db  1802  GAGGAGAGGCCATGCTGGGCCAAGCTGCAGGCGGACTCGGGCCAACTCCATGGAAGGCCTG  1861

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Db  1862  ATGCCACGCTGGGTGCCGGTGCCGGCCGCCTTCTCCCGACCAAGGACTTCCAAGGCTTTCCGC  1921

Qy  1801  CAGATGGGCATTGATGATTCCAGCAAGAGACAACCGGGCGCCACCCCAAGATGCCTGAACCCT  1860
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Db  1922  CAGATGGGCATTGATGATTCCAGCAAAGAGAACAACCGGGCCCAAGATGCCCTGAACCCC  1981

Qy  1861  GAGGAGGATGAGGTGGATGAGTTCCTGGACCGTGCCATGCGCCAGCATTGATCAGCTG  1920
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Db  1982  GAGGAGGATGAGGTCGATGAGTTCCTGGGCCGTGGCATCGATGATCCATCAGCTA  2041

Qy  1921  CGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGGAGATCTTGAGAAGAAG  1980
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Db  2042  CGGAAGGACCATGTGCGCCGGTTCCTGCTCACCTTCCAGAGAGAGGGATCTTGAAAAGAAG  2101

Qy  1981  TACTCCCGGAGGTGGATCCCCGGTTCGGAGGCGCTCAGGTGCCTGTGCCCTTGGTCTTC  2040
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Db  2102  TACTCAAGGAGGTGGACCCCCGGTCGGAGGCCCTGCGGTGCCTGTGCCCTGTTGGTCTTC  2161

Qy  2041  TGCTTCATCTGCTTCAGCTTCCATCTTCCCACTCCACCGTGGCTGCTAATCACCGTGTCTGT  2100
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Db  2162  TGCTTCATCTGCTTTATCCAGCTCCTTCCTGTTCAGTCTTCAGTGTTCAACCTCGATCGTGGATC  2221

Qy  2101  TATGCCAGCATCTTCCTGCTGCTCAATCACGTGTCGATCGTGTGACTCCTGT  2160
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Db  2222  TACGCCAGTATCTTTGTGCTGCTGCTCAATCACCGTGTCGATCACCTGTGCTGTACTCCTGT  2281

Qy  2161  GGTTCTCGTTGTCCCAAGGCCTTCAGGAGGCCATTGTCCGCCTCACGGGGCA  2220
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Db  2282  GGCTCTCTCTTCCCCAAGGCCCTGCGACGTCTTTCCCGGCTCCGCTCGGGGCA  2341

Qy  2221  CATAGCACCGAGTTGGCATCTTTCCGCTCGTGTTTTACTTCTGCCAAC  2280
          || || ||| ||||||||||||| || ||||| ||||  ||||||||||
Db  2342  TGCTTCATCTGGTTGGCATTTTTTCAGTCTTCACCTCTTCCATCGCCAAC  2401

Qy  2281  ATGTTCACCTGTAACCACCACACCCCCACCATACGGAGCCGGATGCTGAATTTAACA  2340
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Db  2402  ATGTTCACCTGTAACCACCACACCCCCATCCGACGGACCGGATGCTGAATGTAACA  2461

Qy  2341  CCTGCTGACACACTCACTGCCACCTGCAGCAGCTCAATTACTTCTGGGCCTGGATGCT  2400
          ||| ||| ||||| |||| ||||||||||||||||||||| |||||||| |||||||||
Db  2462  CCCGCTGACATCACTGCCACCTGCAGCAGCTCAATTACTTCTGGGCCTGGATGCT  2521

Qy  2401  CCCCTGTGTGAGGGCACCATGCCCACCTGCGCAGCTTTCTGCAGTACTTCATCGGGAACATG  2460
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Qy   241  GAGCTCGGGGCTGCGCGGGCAGTGCCCCTGGGCTTTGAGGATACCCGGAGTGACAACGACAGCG  300
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Db   368  GAGCTCGGGGCTGCGCGGGCGGTGCCCCTGGGCTTCGGGCCTTCGAGG---CCATGTCAGCG  424

Qy   301  GGCGGGACGGCTGAGGTGCGCGCCCGACGCGTGGGCCGGATCCTCGTTGGCGC  360
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Db   425  GTTGGGGACGGCAGCTGAGGTGACAGTGGCGCCCCTGACGCCCGGGAGTAGGCGGCCTGCGGCGC  484

Qy   361  CGTCTGGTGCAGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC  420
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Db   485  CGTCTGGCCCAGGTGTTCCAGTGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTAC  544

Qy   421  CAGCGGTACTTCTTCAGATGAACCAGAGACGCCTGACGCGTGCTGATGGGCGTGTGGTG  480
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Db   545  CAGCGGTACTTCTTTCAGATGAACCAGAGACAGCCTGACGCGTGCTGATGGGCGTGCTGGTG  604

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Qy   601  CATAGTTCCGCCAGGACTCCATGTGGTGAGTTACGTGGTGTGGGCATCCTGGCG  660
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Db   725  CACAGCTTCGCCAGGACTCCATGTGGTGAGTTACGTGGTGTGGGCATCCTGGCA  784

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Db   785  GCCGGTTCAGGTTGGGGGTGGGGTGCCCTGGCAGCCAACCCCCGCAGCCCCGTGTGGGCCTCTGG  844

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Qy   781  GTCCTCAGCCGGCCTGGGCCTCTCCACCTTGATCTTGGCCTTGGCCAACTTAACCGT  840
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Db   905  GTCTTCAGTGCCGGCCTGGGCCTGTCCACCTTTGATCTTGGCCTTGGCCAACTCAACCGC  964

Qy   841  GGTGATGCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTCGTGTTCCTGCTCCGCACCAAC  900
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Db   965  GGTGAGAGCCTTCCTCTGGAAGCAGCTCGGTGCCAACATGTCGTGTTCCTGCTCCGCACCAAC  1024

Qy   901  GTCATTGGCATCTGCACACACTATCCACAGAGTTCTCACGCGCCTTTCAGCATC  960
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Db  1025  GTCATTGGCATCTGCACACACTACCCACAGAGTCTCTCACGCGCCTTTCAGCATC  1084

Qy   961  ACCCGGCGGTTACATCCAGCGGCCCCGGGCTTCACCTGCAGCATGAGAATCGGCAGGAGGCGG  1020
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Db  1085  ACCCGGCGGTTACATTCAGGCGGCCCCGGGCTGCACCTGCAGCATGAGAACGGCAGCAGGAGCGG  1144

Qy  1021  CTGCTGCTCGGTATTGCCCCAGCACGTTGCCCATGGCCATGGAGGATGAAAAGAGACATCAACACA  1080
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Db  1145  CTGCTGCTCTGGAGATGTGCCCCAGCAGCGTTGCCCATGGAGGATGAAAAGAAGAAGATATCAACACA  1204

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Db  1205  AAGAAAGAAGACATGATGTTCCACAGATCTACATCCAGAGCATGACAATGTCAGCATC  1264

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Qy  1261  CTTGCAGTGACTGGGGGACTGTTACTACGTGTCAGGGGCTGCCCGGGGCCCCGG  1320
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Db  2762 TTTGATGGGCTGGACTGTCCCCCAGCTGCGGGGAGGGTGGCACTGAAATACATGACCCCTGTG 2821

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Qy  2821 CAGGCATACAACCGGAGCGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTC 2880
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Qy  2881 CTGGCCCCGGGAGCGGCCGCCAATGATGAACTTCTACTATCAGTCGTGTGAGTGGTGGCGTGTT 2940
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Db  3122 GGTGTCGAGTGCGCTGCTGCGGCGCTGCTCAACGAGATCATCGCCGTGACTTTGATGAGATCATCAGC 3181

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Db  3182 GAGGAGCGCGTTCCGGCAGCTGGAGAAAATCAAGACGATCGCCGTAGCACGTACATGGCGTGCG 3241

Qy  3121 TCAGGGCTGAACGCACCTAGGATCAGGTGGCCGCGTCCCCACACATCGCCCTGGCT 3180
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Db  3242 TCGGGGCTGAACGCGACCACCTACGATCAGGCCGCCGCTCCCACATCACTGCCCTGGCC 3301

Qy  3181 GACTACGCCATGGCCATGCGGCTCATGGAGCAGGAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
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Db  3302 GACTATGCCATGGCCATGCGGCTCATGGAGCAGGAGATGAAAACACATCAACAAGCACTCCTTCCTTCAACAAC 3361

Qy  3241 TTCCAGATGAAGATTGGGCTGAACATGGCGCCCAGTCGTCGTGGCCAGCTGCTGGGGCTCGG 3300
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Db  3362 TTCCAGATGAAGATTGGGCTGAACATGGGCGCCCAGTTGTGCGCAGGCGTCATTGGGGCTCGG 3421

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Db  3422 AAGCCACCACATGATGCATCTCGGGGAACAGTCGTGGGGAACAGTGATCTTCTTAGCCGTGGACAGCACG 3481

Qy  3361 GGGGTCCCGACCGAATCCAGTGACCAGGTTCTACCAGGTTCAGCTGCCAAGGGC 3420
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Db  3482 GGGGTTCCTGACCGGAATCCAGTGACCAGGTTCTACCAGGTTCTACCAGGTTCAGCTGCCAAACGG 3541

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Qy  3541 AAGGTGGGCACT 3552
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Db  3662 AAGGTGGGCATT 3673
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RESULT 5
US-08-726-214-11
; Sequence 11, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-726-214-11

Query Match   79.1%;   Score 2810.4;   DB 3;   Length 4131;
Best Local Similarity   87.5%;   Pred. No. 0;
Matches 3110; Conservative 0; Mismatches 436; Indels 8; Gaps 3;

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Db  173 CCCGGCTACATGAGCTGCCTCAAGAATGTGGAGCCCCAGTCCCAGCACCCCACTCCTGGCAAGGGCCAGG 232

Qy  181 CCTCGGTGCCCTGCAGGATGACGCCTTCATCCTGGAGGGGCCCAGGGGCCAAGGCAAG 240
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Db  233 ACTCGGTGCCCTGCCAGGATGACGCCTTCATCAGGAGGATGAACCTTCTCGGGCTTCGAGGAGGGGGTGTG 292

Qy  241 GAGCTGGGGCTGCCGGCAGTGGCCCTGGTGCTTCGAGGATATCCGAGGTGACAACGACAGCGC 300
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Db   293 GAGCTGGGGGCTGCGGTCAGTGCCCTGGGTTTGATGACACTGAGCTG---ACCACACCG 349
Qy   301 GGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGGTGGGCGGATCCTGCTGCGC 360
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Qy   361 CGTCTGGTGCGAGGTGTTCCAGTGCAGTTCCGGTTCGGCCGCAAGCTGGAGCGCCTGTAC 420
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Qy   481 CTGCTCCAGCGGTGCTGCTGCTTCCACGCGCACCCGCCCGCCCCCAGCCCTGCTAT 540
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Qy   541 GTGGCACTGGTTGGCCGTGCGCGCCCGTGTTCGTGGGGCTCATGGTGTGTGTAACCGG 600
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Qy   601 CATAGCTTCCCGGCCAGAGACTCCATGTGGGTGGTGAGTTACGTGGTGCTGGGCATCCTGGGCG 660
Db   650 CATAGCTTCCCGGCCAGAGACTCCATGTGGGTAGTGAGCTATGTGGTTCTGGGCATCCTAGCA 709

Qy   661 GCAGTGCAGGTCGGGGGCGCTCTCGACGCAGCACCCGCCAGCCCCTGCTCCTGCGGGCCTCTGG 720
Db   710 GCCGTGCAAGTCGGGGGTGCCCGGGCTCTGCTGAGCAGCCCACGCAGCCCTCAGCCCCTTTGG 769

Qy   721 TGCCCTGTGTTCTTGTCTCTGGTACATGCCTACATGGCCTACCTCCCCATCCGGCCATGCGGGCTGCC 780
Db   770 TGCCCCGTGTTCTTGTCTCTGGTACATCCTACATCCTCCCCATTCTCCTGGTGTGTGCGGGGCC 829

Qy   781 GTCCTCAGCCGGCCCTCGGGCCTTTGCCTGGCCTGCATTGATCTTGGCCTGGCCAACTTAACCGT 840
Db   830 GTGCTCAGTGGCCTGGGCCTTTTCCACCCTGACTCCCTGCATTTGATTTTTGGCCATCTCAACAAT 889

Qy   841 GGTGATGCCTCCTCCTGGAAGAGCTCGGTGCCCAATGTGCTGGCCAATGTGCTCGTGTCTCTGCACCAAC 900
Db   890 GGTGACCCCTTCCTTTGGAAGCAGCAGCTCGGTGCTCAACGTGGTCTGGCTACGTGTGCTCTCCTGCTGTGCACCAAT 949

Qy   901 GTCATTGGCATCTGCACACACTATCAGCAGAGGTGTCTCAGCGGCCTTCAGGAG 960
Db   950 GCCATCGGTGTCTGCGCACGCGCACCTACCTCCGGCCTCCCAAGCCTTTCAGGAG 1009

Qy   961 ACCCGGCCGTGGGTTACATCCAGGCCCCGGCCTTCAGCAGATGAGAATGGCAGCAGGAGCGG 1020
Db 1010 ACCCGGTGGTTACATCCAGGCGCCGGCTGCACTTGCAGCATGAGAATCGACAGCAGGAACGG 1069

Qy 1021 CTGCTGCTGTCGGTATTGCCCATGCTTGCCATGGCCATGGATGAGAGATGAAAGAAGATCAACACA 1080
Db 1070 CTGCTGCTGTCGGTGTTGCCCCCAGCATGTTGCCATGGCCATGGGATGAGAATGAAAGAGGATATCAACACA 1129

Qy 1081 AAAAAGAAGACATGATGTTCCACAAGATCTACATCAGAAGCATGACAATGTCAGCATC 1140
Db 1130 AAAAGGAAGACATGATGTTCCACAAGATTTACATCAGAAGCATGACAATGTCAGCATC 1189

Qy 1141 CTGTTTGCAGACATTGAGGGCTTCACCAGCGCATCCCAGCGCTGCGCTGCAGGAGCTG 1200
Db 1190 CTGTTTGCCGACATCGAGGGCTTCACCAGCGCCTCCCAGCTGCGCTGCGCCCAGGAACTG 1249

Qy 1201 GTCATGACCCTGGAATGAGCTTTGCAAGGCTGGCTGCGAGAATCACACTGT 1260
Db 1250 GTCATGACCTTGAATGAGCTTAGGAGACTGGGCTTGCGACAAGCTGCCGGAGGCCCGG 1309

Qy 1261 GTCAGGATCAAGATCTTGGGGGACTGTCTACTGTCGTCAGGGGAAATCACTACGT 1320
Db 1310 CTGAGGATCAAGATCTTAGGAGACTGTTACTGTGTGTCGGGGGCTGCGGAGGCCCCGG 1369

Qy 1321 GCCGACCATGCCCAACTGCTGTGTGGAGATGGGGTTAGACATGATTGAGGCCATCTCGCTG 1380
Db 1370 GCAGAGACCATGCCCACTGCTGTGTGTGAGAGATGGGGGTAGACATGATTGTGTCGAGCCATCTCGCTG 1429

Db 1381 GTACGTGAGGTGACAGGTGTGAATGTGAAACATGCGCGTGGGCATCCACAGCGGGCGCGTG 1440
Qy 1430 GTGCGTGAGGTAACGGGTGTAAAATGTGAACATGCGGGCGGGCATCCACAGCGGGCGGGTGTA 1489

Db 1441 CACTGCGGCGTGTCCTTGCTGCTGTCTGCGGAAATGGCAGTTGATGTGTGTCCAATGATGTGACC 1500
Qy 1490 CACTGCGGCGTGTCCTTGGTCTGCGGAAATGGCAGTTGATGTCTGGTCCAACGATGTGACC 1549

Db 1501 CTGGCCAACCACATGGAGGCAGGAGGCCGGGCTGGCCGCATCCATCACTCGGGCAACA 1560
Qy 1550 CTGGCCAACCACCATGGAGGCAGGAGGCCGGGCCGGGGGCATCCATCACTCGGGCCACA 1609

Db 1561 CTGCAGTACCTGAACCGGGGACTACGAGGTGAGCCAGGCCGTGGTGCGGCAGCGGCAACGCG 1620
Qy 1610 CTGCAGTACCTCAACCGGGGGACTATGAGGTGGAGCGTGGAGCCCGTGGGCGGAGCGCAACCCG 1669

Db 1621 TACCTCAAGGAGCAGCACATTGAGGACTTTCCTCATCTCCATCCTGGGCGGGACTCGGAACCCT 1680
Qy 1670 TACCTCAAGGAGCAGCAGTGCATTGAGACCTTCCTCATACTAGGAGCCAGCCAGAAAACGGAAA 1729

Db 1681 GAGGAGGAGGCCATGGTGGCCAAGCTGCAGCGGACTCGGCCGGCCAACTCCATGGAAGGGCTG 1740
Qy 1730 GAGGAGGAGGCCATGTGGGTGGTCAAGCTGTGGTCAGCAGTTCTCGGCGGCCGGCCGCAACTCCATGGAAGGACTG 1789

Db 1741 ATGCCCGGCTGGTTCCTGATCGTGTGCCTTCTCCCGGACCAAGGACTTCCAAGGCCTTCGC 1800
Qy 1790 ATGCCCGGCTGGTGGGTTCCTGACGTGCCGTCCTGCCTGCCTCCGGACCAAGACCTAAGGCCATTCCGA 1849

Db 1801 CAGATGGGCCATTGATGATTCCAGCAAAGACAACACCGGGGCACCCAAGATGCCCGAACCCT 1860
Qy 1850 CAGATGGGCATCGATGATACTCTAGCAAAGAACACCGGGGTGCCCAAGATGTCTGAACCCT 1909

Db 1861 GAGGATGAGGTGGATGAGTTCCTGCGCCGTGCCATCGATGATGCCGAGCATCATCGACCAGCTG 1920
Qy 1910 GAGGAGGAGGTGGACAGGTTCTCGGGGCCGCGTGCCGCCATGATGCCGAGGCATCGACCAGCTG 1969

Db 1921 CGGAAGGACCATGTGCGCCCGGTTTCTGCTCACCTTCTGCTGCCTTCCGAGAGAGAAG 1980
Qy 1970 CGTAAGGACCATGTGCGCCGGTTCCTGCTCTCACCTTCCAGAGGAGCATCCGAGAAGGAAG 2029

Db 1981 TACTCCCGGAAGTGGATCCCCGTCCGGAGGCTACGTTGCCCTGTTGGTCTTC 2040
Qy 2030 TATTCACGGAAAGTAGACCCTCGTTTCGGAGCTACGTGCCGCTGTGCCCTGTTTTTC 2089

Db 2041 TGCTTCATCTGCTTCATCAGCTTCATCTTCCCACACTCCACCTTGGGATC 2100
Qy 2090 TGCTTCATCTGCTTCATCAGCTTCATCTTCCCACACTCCACCTTGGGATT 2149

Db 2101 TATGCCAGCATCTTCCTGCTGCTGTCTAATCACCGTGTCGTGTGTGTACTCCTGT 2160
Qy 2150 TATGCCCGGGATCTTCCTTTTGCTGCTGTCTCATCTGTCGTGTGTGTCTCCTGT 2209

Db 2161 GGTTCTCTGTCTCCCTAAGGCCCCTGCAACGTGTCTGCCGCCATTGTCCCGCTCACGGGCA 2220
Qy 2210 GGGTCTTTCTTCTTCCCCAACGCCCTGCAGCCCGTGTCGCAGTATCCGCTCACGGGGTG 2269

Db 2221 CATAGCACCGCAGTTGGCATCTTTTCCCGGCATCTTTTACTTCTGCCAAC 2280
Qy 2270 CACAGCACGGCGTGTTGCAGCTGTTTCTCGGTTCGTTGTTTCATCTCTGCCAAC 2329

Db 2281 ATGTTCACCTGTAACCACACCACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAACA 2340
Qy 2330 ATGTTCACCTGTAACCACACCATCGTGCGGGATGAGATCAAGACTCAACATCTTTGAATTGGCCAGA 2389

Db 2341 CCTGCTGACATCGAAGCTGCCGCTGCCACCGAGCAGCTTTTCCTGGGCCCTGATGCT 2400
Qy 2390 CCGTCCGATGTCCAGTGCACCGCGCTGCCACTACGACGCTCAATTACTCTCTGGGGACTGGAAGCT 2449

Db 2401 CCCCTGTGTGAGGGGCACCATGCCCCAGCTTTCCTGGCACTTCATCGGGAACATG 2460
Qy 2450 CCCCTGTGTGAGGGGCACCCACCGCGCTGCCCGCTGCTTCCCTGAGTACTTTGTGTCGGGAGTGTG 2509

Db   3590 CCAAGGTGGGCACT 3603
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RESULT 6
US-09-008-097-3
; Sequence 3, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1812
; OTHER INFORMATION:
US-09-008-097-3

Query Match   49.6%; Score 1763.4; DB 4; Length 1812;
Best Local Similarity   98.7%; Pred. No. 0;
Matches 1789; Conservative   0; Mismatches 21; Indels   3; Gaps   1;

Qy   636 TTACGTGGTGCTGGGCATCCTGGCGGCCAGTGCAGGTCGGGGCGCCTCTCCGCAGCAGACCC 695
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3 TAACGTGGTGCTGGGCATCCTGGCGGCCAGTGCAGGTCGGGGCGCCTTTCCGCAGCAGACCC 62

Qy   696 GCGCAGCCCCTGCTGGCCTCTGGTGCCCTGTGTTCTTTGTCTACATCGCCTACCACGCGT 755
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 GCGCAGCCCCTGCTGGCCTCTGGTGCCCTGTGTTCTTTGTATACATCGCATACACGCGT 122

Qy   756 CCTCCCCATCCGCATGCGGGCTGCCTGGGCCTGGCCTTCCACCTTGCATTT 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 CCTCCCCATCCGCATGCGGGCTGCCTGCGTCCTCCGCGGCCTGGCCTTCCACCTTGCATTT 182

Qy   816 GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCTGGAAGCAGCAGTCGGTGCCAA 875

Qy   2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCGACATCAGCAGCATCGGGAAGTTGGCC 2520
          |||||||||||||| |||||||||||||||||||||| ||||||| ||||||||||||| |
Db   2510 CTGCTGAGTCTCTTGGCCAGCTCCGTCTCCTCCTCCACCAGCATTGCAAGCTAGTT 2569

Qy   2521 ATGATCTTTGTCTTGGGCTCATCTATTGGTGTGCTTCTTCGTCCCCAGCCACC 2580
          |||| ||||||| ||| |||||||||||||||||| |||||||||||||||||||
Db   2570 ATGACCTTTGTCTTGTCTGGGGTTCATCTACTTGCTTCTGCTTTGCTGGGTCCCCAGCCACC 2629

Qy   2581 ATCTTTGACAACTATGAACTTGCTTGGCGTCTGGCTTCTTCCAATGAGACC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2630 ATCTTTGACAACTATGATCTTGCTTGGCGTCTGGCTTCCTCCAATGAGACC 2689

Qy   2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATGACCCCCTGTG 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2690 TTCGATGGGCTGGACTGCCCCAGCCGTCAAATATGACACCCCTGTG 2749

Qy   2701 ATTCTGCTGTGTTGCGCTGGCGGCTGGTCGATCTGCAATGCTCAGCAGGTGGAGCTGCC 2760
          |||||| ||||| ||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2750 ATTCTCCTCGTGTTCGCCCTGGCACTGTATCTCACACGCACAACAGGTGGAATCTACCGCC 2809

Qy   2761 CGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGAGAAGGAGGAGGAGGAGCTA 2820
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   2810 CGCCTGGACTTCCTGTGTGAAACTGCAGGCCACAGGGAGAAGGAGGAGGAGGAGAGTTG 2869

Qy   2821 CAGGCATACAACCGGAGCGCTGCTGCATAACATTCTGCCCAAGACGTGGCGGCCCACTTC 2880
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   2870 CAGGCCTACAACCGGCGCGCTGCTGCATCATCCTTCCCAAGACGTGGCCCACTTC 2929

Qy   2881 CTGGCCCGGGAGCGCGCCGCAATGAGATGAACTCTACTATCAGTCGTGTGGCTGTT 2940
          ||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||||
Db   2930 CTGGCCCGGGAGCGCGCCGCAACGAGCTGTACTACCAATCCTGCAGTGCGTGGCTGTC 2989

Qy   2941 ATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAG 3000
          |||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||
Db   2990 ATGTTTGCCTCCATCGCCAACTTCTCTGAGTTCTATGTGGAACTGGAGGCGAACAATGAG 3049

Qy   3001 GGTGTCGAGTCGCCTGCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060
          || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   3050 GGCGTGGAGTCGCCTGCGACTGCTCAATGAGATCATCGCGGACTTTGATGAGATCATCAGT 3109

Qy   3061 GAGGAGCGCGGTTCCGGCAGTCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCC 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3110 GAGGAGAGGTTCCGGCAGTCGGCAGCTGGAGAGAATCAAGACCATCGTAGCACTTACATCGCCCGCC 3169

Qy   3121 TCAGGGCTGAACGCCAGCACCTACGATCCAGGTGGGCCGGTCCCACCACTCGCCCTGGCT 3180
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   3170 TCCGGGCTAAATGCCAGCACCTATGACCACAGGTGGCCCGCTCGGCACATCACCGCCCTGGCA 3229

Qy   3181 GACTACGCCATGCGGCTCATGGAGCAGAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
          ||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||
Db   3230 GACTACGCCATGCGGCTTATGGAGCAATAAATGAAAACACATCAACGAACACACTTCTTTCAACAAC 3289

Qy   3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTTGGCAGTGTCATCGGGGCTCGG 3300
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   3290 TTCCAGATGAAGATCGGGTTGAACATGGCTCCGGTTGTAGCAGTGTCATTCAATGGGGCCCGG 3349

Qy   3301 AAGCCACAGTGATGACATCTGGGGGAACACTCGGGGAAACAGTGAATGTCTCTAGTCGTATGGACAGCACG 3360
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   3350 AAGCCACAGTGATGACATCTGGGGGAAACACGGTGAATGTTTCCAGCCGGTATGGACAGCACA 3409

Qy   3361 GGGGGTCCCCGACCGAATCCAGTGACCCGACCTGTTACCACGGTTCAGCCAAGGGC 3420
          |||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   3410 GGAGTTCCTGACCGAAATACAGGTGACCACGGATCTCTCACCAGGTTCAGCCAAGGGC 3469

Qy   3421 TACCAGGTGGAGTGTCGAGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTAC 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3470 TACCAACTGGAGTGTCGAGGGGTCGTCAAGGTGGTCAAGGTGAAAGGGGAGATGACCACCTAC 3529

Qy   3481 TTCCTCAATGGGGCCCCCAGCAGTTAACAGGGCCCA--GCCACAAATTCAGCTGAAGGGA 3538
          |||||||||||||||||||||||||||||||| ||| ||||||||||||||||| |||
Db   3530 TTCCTCAATGGGGCGCCCCAGCAGTTAGCAGAGACGCACGAGTTGAAAATTCAACCAAAGGGA 3589

Qy   3539 CCAAGGTGGGCACT 3552

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Db  183  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GATCTTGGCCTGGCAACTTAACCGTGGTGATGCCTTCCTCCTGGAAGCAGCTCGGTGCCAA  242

Qy  876  TGTGCTGCTGTTCCTCGCACCAACGTCATTGGCATCTGCACACTATCCAGCAGAGGT  935
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         TGTGCTGCTGTTCCTCGCACCAACGTCATTAGCATCTGCACACTATCCAGCAGAGGT  302

Db  243

Qy  936  GTCTCAGCGCGCCAGGCCTTTCAGGAGACCCGCGGTTACATCCAGGCCCGGCTCCACTGCA  995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTCTCAGCGCGCCAGGCCTTTCAGGAGACCCGCAGTTACATCCAGGCCCGGCTCCACTGCA  362

Db  303

Qy  996  GCATGAGAATCGGCAGCAGGAGCGGCGGCTGCTGCTGTCGTGGTATTGCCCCAGCAGTTGCCAT  1055
         |||||||||||||||||||||||||||||||||||||||||||||||
         GCATGAGAATCGGCAGCAGGAGCGGCGGCTGCTGCTGTCGTGGTATTGCCCCAGCAGTTGCCAT  422

Db  363

Qy  1056 GGAGATGAAAGAAGACATCAACACAAAAAGAGAGACATGATGTTCCACAGATCTACAT  1115
         ||||||||||||||||||||||||||||||||       |||||||||||||
         GGAGATGAAAGAAGACATCAACACAAAAAGAGAAGAC---ATGTTCCACAGATCTACAT  479

Db  423

Qy  1116 ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC  1175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGC  539

Db  480

Qy  1176 ATCCCAGTGACACTGCGCAGGAGCTGGTCATGAGCTCTTTGCCCGGTTTGA  1235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATCCCAGTGACACTGCGCAGGAGCTGGTCATGAGCTCTTTGCCCGGTTTGA  599

Db  540

Qy  1236 CAAGCTGGCTGCGGAGAATCACTGCCTGAGATCAAGATCTTGGGGGACTGTTACTACTG  1295
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAAGCTGGCTGCGGAGAATCACTGCCTGAGATCAAGATCTTGGGGGACTGTTACTACTG  659

Db  600

Qy  1296 TGTGTCAGGGCTGCCGGAGGCCCGGCCCGGCCGGCCGACCATGCCACTGCTGTGTGTGGAGATGGGGGT  1355
         ||||||||||||||||||||||||||||||||||||||||
         TGTGTCAGGGCTGCCGGAGGCCCGGCCCGGCCGGCCGACCATGCCACTGCTGTGTGTGGAGATGGGGGT  719

Db  660

Qy  1356 AGACATGATTGAGGGCCATCTCGCTGCTACGTGACGAGGTGTGAATGTGAACATGCG  1415
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Db  720

Qy  1416 CGTGGGCATCCACAGCGGGCGGGCGTGCACTGCGGGCGTCCTTGGCTTGCGGGAAATGGCAGTT  1475
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  780

Qy  1476 CGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACCATGGAGGCAGGAGGCCGGGCTGG  1535
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         CGATGTGTGGTCCAATGATGTGACCCTGGCCAACCACCATGGAGGCAGGAGGCCGGGCTGG  899

Db  840

Qy  1536 CCGGCATCCACACTCACTCGGGGCAACACTCCAGTACTCGAACGGGGACTACGAGGTGGAGCC  1595
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         CCGGCATCCACACTCACTCGGGGCAACACTCCAGTACTCGAACGGGGACTACGAGGTGGAGCC  959

Db  900

Qy  1596 AGGCCCGGTGCGAGCGCAACGCGCAACGCGTACCTCAAGGAGCAGCAGCATTGAGACTTTCCTCAT  1655
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         AGGCCCGGTGCGAGCGCAACGCGCAACGCGTACCTCAAGGAGCAGCAGCATTGAGACTTTCCTCAT  1019

Db  960

Qy  1656 CCTGGGGCGCCAGCCAGGAAACGGAAAGAGGAGAAAGGAGCATGCTGGCCAAGCTGCAGCGGAC  1715
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         CCTGGGGCGCCAGCCAGGAAACGGAAAGAGGAGAAAGGAGCATGCTGGCCAAGCTGCAGCGGAC  1079

Db  1020

Qy  1716 TCGGGGCCAACTCCATGGAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCCCCG  1775
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Db  1080

Qy  1776 GACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAAAGACAACCG  1835
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Db  1140

Qy  1836 GGGCACCCAAGATGCCCTGAACCCTGGAGGATGAGTTCCTGAGCCGTGCCAT  1895
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         GGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCAT  1259

Db  1200

Qy  1896 CGATGCCCGCAGCATTGATCAGCTGCGGAGGACCATGTGCGCCGGTTTGCTCACCTT  1955
         |||||||||
         CGGAGGGGGCGGCCCAGGCCCAGGCCGCAAGGAGCTGGGGCTGCGGGGCAGTGGCCCCTGGGCTTC  273
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Db  1260 CGATGCCCGCAGCATTGATCAGCTGCGGAGGACCATGTGCGCCGGTTTTGCTCACCTT  1319

Qy  1956 CCAGAGAGAGATCTTGAGAGAGAAGTACTCCCGGAGGTGGATCCCGGCTTCGGGAGCCTA  2015
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1320 CCAGAGAGAGATTTGAGAGAGAAGTACTCCCGGAGGTGGATCCCGGCTTCGGGAGCCTA  1379

Qy  2016 CGTTGCCTGTGCCCTGTTGGTCTTCGTCTTCATCGTGCTTCATCCAGCTTCTCATCTTCCC  2075
         |||||||||||||||||||||||||||||||||||||||||  ||
Db  1380 CGTTGCCTGTGCCCTGTTGGTCTTCGTCTTCATCGTGCTTCATCCAGCTTCTCAATTTTCCC  1439

Qy  2076 ACACTCCACCCTGATGCTTGGGATCTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGT  2135
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Db  1440 ACACTCCACCCTGATGCTTGGGATCTATGCCAGCATCTTCCTGCTGCTGCTAATCACCGT  1499

Qy  2136 GCTGATCTGTGCTGTGTACTCCTGTGTTCTCGTTCCCTAAGGCCCTGCAACGTCTGTC  2195
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Db  1500 GCTGATCTGTGCTGTGTACTCCTGTGTTCTCGTTCCCTAAGGCCCTGCAACGTCTGTC  1559

Qy  2196 CCGCAGCATTGTCCGCTCACGGGCACATAGCACGCGAGTTGGCATCTTTCCGTCCTGCT  2255
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1560 CCGCAGCATTGTCCGCTCACGGGCACATAGCACGCGAGTTGGCATCTTTCCGTCCTGCT  1619

Qy  2256 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCAGCCCCATACGGACTG  2315
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Db  1620 TGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCAGCCCCATACGGAGCTG  1679

Qy  2316 TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGCCACCTGCCAGCAGCT  2375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1680 TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGCCACCTGCCAGCAGCT  1739

Qy  2376 CAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCCAGCTT  2435
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Db  1740 CAATTACTCTCTGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCCAGCTT  1799

Qy  2436 TCCTGAGTACTTC  2448
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Db  1800 TCCTGAGGTGTTC  1812
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RESULT 7
US-09-473-716-1
; Sequence 1, Application US/09473716
; Patent No. 6436672
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James
; APPLICANT: Cor Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5027-01-US
; CURRENT APPLICATION NUMBER: US/09/473,716
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13540
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,901
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,362
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4523
; TYPE: DNA
; ORGANISM: human type V adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)..(3921)
US-09-473-716-1

Query Match   49.6%; Score 1761; DB 4; Length 4523;
Best Local Similarity 72.2%; Pred. No. 0;
Matches 2385; Conservative   0; Mismatches 885; Indels 33; Gaps   6;

Qy 214 CGGAGGGGGCGGCCCAGGCCCAGGCCGCAAGGAGCTGGGGCTGCGGGGCAGTGGCCCCTGGGGCTTC 273

Left alignment block:

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Db   625 |||  |||||                                  ||| |||||||
         CGGCGGGCAAGGGCGCGGCCACGAGCTGGAGGCCGGCGAG  684
Qy   274 GAGGATACCGAGTGACAACGACAGCGGGGACGGCTGGAGGTGGCGCCGACGCGGTG  333

Db   685 GGGTCCGGGGATGGCGGCAGCTCGGCGGACTCGGCGTCCGGGGCCGGGGTG  744
Qy   334 CCCAGGAGTGGGGCGATCGTCTCGGCCCGTCGTGGTCAGTGTTCCAGTCGAAGCAGTTC  393

Db   745 C---TGTCCCTGGGGCTGCCTGGCGTTGCTGCGATATTCCGCTCCAAGAAGTTC  801
Qy   394 CGTTCGGCCAAGCTGGAGCGCCCTGTACCAGCGGTACTTCTTCAAGATGAACCAGAGCAGC  453

Db   802 CGGTCGGACAAACTGGAGCGCGGCTGTACCAGCGCTACTTCTTCCCGCTGAACCAGAGCAGC  861
Qy   454 CTGACGCGTGCTGATGGCGGTGCTGGTGCGTGCTCACAGCGGTGCTGCTTTCCACGCC  513

Db   862 CTCACCATGTCATCGCCGTGCTGTCTGTGTGCGTTGGCCTTCCACGCG  921
Qy   514 GCACCCGCGCCCTCAGCGCCTGCCTATGTGGCCACTGTTGGCCGTCGTGTTC  573

Db   922 GCGCGGCCCCCGCTCCAGCTGCCGCCCTCACCTGGCGCGGCCGCCGTCGGGCTGATC  981
Qy   574 GTGGGGCTCATGGTGGTGTTGTAACGGCATAGCTTCCGCCAGGACTCCCATGTGGGTGGTG  633

Db   982 CTCATCATGGCTGTGTGCTTTGCAACCGCGCCCTTCCACCAGGACCACATGGGCCTGGCC  1041
Qy   634 AGTTACGTTGGTGCTGGGGCATCCTGGCGCGCAGGTCGGGGCGCTCTGGAGCAGCAGAC  693

Db  1042 TGCTATGCGGCTCATCGCCGTGGTGTCGCCGTCTGGCGTGTGGCCGTCTGCTGCCGCAG  1101
Qy   694 CGGCGCAGCCCCTCTGGGGTGCCCTGTGTTCTTGTTCTTGTCTACACG  753

Db  1102 CCACCAGCGCGCCCTCTGAGGCGATCTGGTGACCGTGTTCTTCATCTACACCATCTACACG  1161
Qy   754 CTCCTCCCCATCCGCATGCGGGGCTGCCCGGTCGGTCCGTCCTGGCCTCTCTCCACCTTGCAT  813

Db  1162 CTGCTGCCCGGTGCCCATGCGGGGCCGCCGCAGTGCTCAGCGGGGCGTGCTCCGCCCTCCAC  1221
Qy   814 TTGATCTTGGCTTGGCAACTTAACCGTGGTGATGCCCTTCCTGGAAGCAGCTCGGTGCC  873

Db  1222 CTGGCCATCGCCGTGCGCAGCACCAGTTCCTGCTGAAGCAGCTTGTCTCC  1281
Qy   874 AATGTGCTGCTGTTTCCTCTGCCACCAACGTCATTGGCATCTATCCAGCAGAG  933

Db  1282 AATGTTCTCATTTTCTCTGCACCAACATCGTGGGGTGTCTGCACCCACTATCCGGCTGAG  1341
Qy   934 GTGTCTCAGCGCCAGCCCTTCAGGAGACCGGTTACATCCAGGCCTCCACCTG  993

Db  1342 GTCTCCCAGAGACAGGCTTTCCAGGAGACCCGCATCCAGGCGCGGCTTCCACTCG  1401
Qy   994 CAGCATGAGAATCGGCAGCAGCGCGGCTGCTGTCGTGGTATTGCCCGCACACGTTGCC  1053

Db  1402 CAGCGGGAACCCAGCACAGCAGCACACGGCGTCCTCCTGCGTGTCGTGCTGCTGCC  1461
Qy  1054 ATGAGAGATGAAAGAAGAAGAAGCAATCAACACAAAAAAGAAGAACATGATGTTCCAAGAGATCTAC  1113

Db  1462 ATGGAGATGAAAGCAGACAATGACAACGTGAGCATCTGTTTGCTGACATTCCATARAGATTTAC  1521
Qy  1114 ATACAGAAGCATGACAATGCACAGTGTCAGGGCTTCACCAGCCTG  1173

Db  1522 ATCCAGAAACATGAACGACAACATCAACGCTGTTTGCTGACATCGAGGGGCTTCACCAGCCTG  1581
Qy  1174 GCATCCCAGTGCACTGCCGCAGAGCTCTTTGCCCGGTTT  1233

Db  1582 GCGTCCCAGTGCACTGCACAGGAACTGGTCATGACAGAGCTTCTTCGCCCGGCTTT  1641
Qy  1234 GACAAGCTGGCTGCCGGAGGATCAAGATCTTGGGGACTGTTACTAC  1293

Db  1642 GACAAGCTGGCGCTGCTTGGCACAGGAGCAACATCAGCCGAGCCAGTCAACGCGTGT  1701
Qy  1294 TGTGTGTCAGGGGCTGCCCGGAGGCCCGACCATGCGCCGATGCTGTGTGGAGATGGGG  1353
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Right alignment block:

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Db  1702 TGCGTCTCGGGGCTGCCTGGGAAGCAAGGGCTGACCACGCCCACTGCTGTGTGGAGATGGGC  1761
Qy  1354 GTAGACATGATTGAGGCCATCTCGGCTGGTACGTGGAGGTGACAGGTGAATGTGAACATG  1413

Db  1762 ATGGACATGATCGAGGCCATCTCGTTGGTCCGGGAGGTGACAGGGGTGACGTGAACATG  1821
Qy  1414 CGGGTGGGCATCCACAGCGGGCGGCGTCCTTGGCTGGTGCGCCGTCTTGCGGGAAATGGCAG  1473

Db  1822 CGTGTGGGGAATTCACAGCGGGGGAGTACACTGGTGCTCCTGGTCTCCAGGAAGTGGCAG  1881
Qy  1474 TTCGATGTGTTGGTCAATGATGTGACCCTGGCCAACCATGGAGGCAGGAGGCCGGGCT  1533

Db  1882 TTTCGACGTCTGGTCTTAACGATGTCACGCTAGCCAACCATCAGAGCCTGGCGGCAAGGCA  1941
Qy  1534 GGCCGGCATCCACATCTGGGCAACACTGCAGTACCTGCAGTACTCGGAACGGGGACTACGAGGTGGAG  1593

Db  1942 GGACGGCATCCACATCCACAAGGCTACACTCAACTACCTGGAATGGGGACTACGAGGTGGAG  2001
Qy  1594 CCAGGGCCGGTGGTGGCGAGGCCAACGCGTACCTCAAGGAGCACAGCAGCACATTGAGACTTTCCTC  1653

Db  2002 CCAGGCTGTGGGGGGCGAGGCCAACGCACCAGTATCGGAGACCTTCCTC  2061
Qy  1654 ATCCTGGGGCGCCAGCCAGCAGGAAAGGAACGGAAAAGGAGAAGGCCATGCTGGCCAAGCTGCGCAGCCGG  1713

Db  2062 ATCCTGGCGCTGCACCCGAGAGCGGAAAGAAGAGAGGCCATGATCGCCAAGATGAACCGC  2121
Qy  1714 ACTCGGGCCAACTCCATGAAGAGCGTGATGCCGTGCTGGGTTCCTGATCGTCCTGCCTCTCC  1773

Db  2122 CAGAGAACCAACTCCATCGGGCACAACCCACCACACTGGGGGGCTGAGCCGCCCCTTCTAC  2181
Qy  1774 -----------CGGACCAAGGACTCCAAGGCTTCCGCCGAGATGGGCATTGATGATTCC  1821

Db  2182 AACCACCTGGGTGGCAACCAGGTGTCGACTTAGAGAGAAGTAGTAGACCCC  2241
Qy  1822 AGCAAAGACAACCGGGGCACCCAAGATGCCTGAACCCTGAACCCTGAGGATGAGGTGGATGAGTTC  1881

Db  2242 A-----AGGACAAGAACGCCCAGGAGGTGCGGAACCCTGAGGATGAAGTGGATGAGTTT  2295
Qy  1882 CTGAGCCGTGCCATCGATGCCCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGG  1941

Db  2296 CTGGGCCGTGCCGTTGCCATTGACGGCCAGGACATTGATAGGCTTCGGTCTGAGCACGTCCGCAAG  2355
Qy  1942 TTTCTGCTCACCTTCCAGATGAGCATCCCGGAAGGTGGATCCC  2001

Db  2356 TTCCTCCTGACCTTCAGGGAGCCTGACTTAGGAGGAAGAGTACTCCAAGCAGGAGACGAC  2415
Qy  2002 CGCTTCGGAGCCTACGTTGCCTATGTGGCGCTGCCTCCGCCGTCCGTCGTTCATCCTCATCCCAG  2061

Db  2416 CGATTTGGTGCCTATGTGGCCTATGTGGCCTCTGTTCATCTGTTCATCTGTTTGTCCAG  2475
Qy  2062 CTTCTCATCTTCCCACACTCCCACCCTGATGCTTGGGATCATCGCCACCATCTTCCTGCTG  2121

Db  2476 ATCACCATCGTGCCCCACTCCACTATTCATGCTCAGCTTCTTCACCTTGTTCCCTGCTG  2535
Qy  2122 CTGCTAATCACCGTGCTGCTGATCGTGTCTCGTGTACTCCTTGGTTCTTCATCCCAG  2181

Db  2536 CTGACCTTGGTGGTGTTTGTTGTTTCCTCCAGGAAGCTCTTCTCGCGGTAAAGCTCTTCCCCCCA  2595
Qy  2182 CTGCAACGTCTGTCCGCGGCCATTGTCCGCTCACGGGACATAGCACCCAGTTGGCATC  2241

Db  2596 CTGCAGACCGTCTGTCGCGGCGATTGTGCCGTCGTCCAACATGAACAGCACCCGGTTGGGGTG  2655
Qy  2242 TTTTCCGTCGCTGTGTTTTACTTCTGCGCAGCATGTTCCACCACACC  2301

Db  2656 TTCACCATCACCCTGGTGTTTCCTGGCGGCTTTGTCAACATGTTCACGTGCAACTCCAGG  2715
Qy  2302 CCCATACGGAGCTGTGCAGCCCGATGCTGAATTTAACACCTGCTGACATCACTGCCTGC  2361

Db  2716 GACCCTGCTGGGCGCTTGGCACAGGAGCACAACATCAGCCGGCCAGTCAACGCGTGT  2775
Qy  2362 CACCTGCAGCAG-----CTCAATTACTCTCTGGGCCTCAACTACACAGCCTGGGCGATGAGCAGGGGC  2415

Db  2776 CACGTGGCCGGAGTCGGCCCGTCAACTCTGGCGATGAGCAGGGGCCTTCTGTGTGGCAGC  2835
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Qy   3496 CCC 3498
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Db   3910 CCC 3912

RESULT 8
US-08-726-214-9
; Sequence 9, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
;   APPLICANT: Tang, Wei-Jen
;   APPLICANT: Gilman, Alfred G.
;   TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
;   TITLE OF INVENTION: AND USES THEREFOR
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Arnold, White & Durkee
;   STREET: P.O. Box 4433
;   CITY: Houston
;   STATE: Texas
;   COUNTRY: United States of America
;   ZIP: 77210
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/726,214
;   FILING DATE: Concurrently Herewith
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/005,498
;   FILING DATE: 04-OCT-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Highlander, Steven L.
;   REGISTRATION NUMBER: 37,642
;   REFERENCE/DOCKET NUMBER: UTSD:450
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (512) 418-3000
;   TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3924 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-726-214-9

Query Match   47.8%; Score 1696.2; DB 3; Length 3924;
Best Local Similarity   72.2%; Pred. No. 0;
Matches 2288; Conservative 0; Mismatches 853; Indels 30; Gaps 5;

Qy   345 GCGATCCTCGTCTGGGCCGCCGTCGTCGGGTCCGTTGGGCGGTGTTCCAGTCGGAGCAGTTCCGTTCGGCCAA 404
          |||| ||||| ||| ||| |||||| ||||||| ||||||||||||| |||| ||||| ||| |||||| |||
Db   128 GGGCGGCCTGCTGCCTGGCCTTGCTGCGAGATATTCCGCTCTAAGAAGTTCCGTCGGACAA 187

Qy   405 GCTGGAGCGGCCTGTACCAGCGGTACTTCTTCAGATGAACCAGAGCAGCGCTGCT 464
          ||||||||| ||| ||||| ||| ||| |||||| |||||||| |||||||||||
Db   188 ACTGGAGCGTCTGTACCAGCGGTATTTCTTCCGCGCCTGAACCAGAGCAGCCTCACCATGCT 247

Qy   465 GATGGCGGTGGTCGGTGCTCACGCGGTGCTGGCTTTCCACGCCGACACCGCCCG 524
          ||| |||||||||| | ||||| ||||| ||||| |||||||||| ||||||||
Db   248 CATGGCCGTGGTCGTCGTGCGCATGTCCTGGTCATCTCGCTTTCCACGGCCGACGCCCCC 307

Qy   525 CCCTCAGCCTGCCATGCTCGACTCACTGCCCTGGCTGACTACGCCATGCGG 584
          ||||||| ||| |||||| |||| ||||||| | ||||||| ||||||||
Db   308 GCTCCAGGTAGTCTACCTGGCCGTGTTGGCAGCTGCTGTGATCCTTATCATGGC 367

Qy   585 GGTGGTCGTGTAACCGGCCATAGCTTCCCGCCATGTGGGTGGTGAGTTACGTGT 644
          |||| |||| |||| |||||||| || ||||||| || ||||||| |||| |||
Db   368 TGTGCTCTGCAACCGGTCCAGCCTTCCACCAGGACCACCAGGACCACCACCATGCGGCT 427

Qy   2416 ACCATGCCCACCTGCGAGCTTTCCTGAGTACTTCATCGGGAACATGCGCTGAGTCTCTTG 2475
          || ||||||||| ||||| ||| |||| ||| | ||||| ||||| |||| | ||||||
Db   2836 CCCTGCCCAACTGCGAACTCCCCGAGTACTTCACCTACAGCGGTGCTGCTCAGCCTGCTG 2895

Qy   2476 GCCAGCTCTGCTTCCTCCTGCGACATCAGCAGCAGGAAGTTGGCCATGATCTTTGTCTTG 2535
          ||| ||||| ||| ||||||| |||||||| || || |||||||| | ||| |||| |
Db   2896 GCCTGCTCCCGTTCTCGAGATCAGCTGGATCAGCTGGTCATCCGCTCTCATGCTCGGCCATC 2955

Qy   2536 GGGCTCATCTATTGGTGCTCTTCTGCTGTGGCTTGGCTTCTCCCCAGCCACCATCTTTGACAACTAT 2595
          ||||| ||| || | ||| ||||| || | | | |||| |||| |||||||| |||||| |
Db   2956 GAGCTCATCA---CGTGCTCATCGTCGAGGTGCCAGGTGTGCCAGGTGTCACGCTCTTCGACAACGCC 3012

Qy   2596 GACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGACACCTTTGATGGGCTGGAC 2655
          ||||| ||||| |||||||||| || || |||| ||||| ||||||||| ||||||
Db   3013 GACCTGCTGGTCACCGCCAACGCCATAGACTTCTTCA---ACAACGGGACCTCCCAGTGC 3069

Qy   2656 TGTCCAGCTGCGAGGAGGGTGGCCCTCAAATATATGACCCTGTGATTCTGCTGTGTGTT 2715
          | ||||||||| || || |||||| | ||||||| ||| ||||| |||| || ||||
Db   3070 CCTGAGCATGCAACCAAGGTGGCATTGAAGGTGGTGACGCCCATCATCATCTCAGTCTTT 3129

Qy   2716 GCGCTGGCGTGTATCTGCATGCTCAGCAGGTGGAGTGACTGCCCGCCTAGACTTCCTC 2775
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Db   3130 GTGTGTGGCCCTGTACCTGCACGCGCCCAGCAGGTGGAGTGTCCAGTCGACTTCCTC 3189

Qy   2776 TGGAAACTACAGGCAACAGGGGAGAAGGAGATGGAGAGCTACAGCCATACAACCGG 2835
          |||||||| |||||| ||| || | | | |||||||| || ||| ||||||||
Db   3190 TGGAAACTGCAGGCCACAGACGGAGCTGCAGGGCTGCAGCCTACACACCGG 3249

Qy   2836 AGGCTGCTGCATAACATTCTGCCCAAGGACCTGCCGCGCCCACTTCCTGGCCGGGAGCGGC 2895
          | ||||| ||| ||||| ||| ||||||| |||| | | || ||||| | || |||||
Db   3250 CGGCTGCTGCACAACATCCTGCCCAAGGACGTGGCCGCTCACTTCCTGGCCCGCGAGCGCGG 3309

Qy   2896 CGCAATGATGAGACTCTACTATCAGTCGCGTGTGAGTGTGGCTGTGTTATGTTTGCCTCCATT 2955
          ||| ||||| ||| ||||| |||||| |||| ||||| ||||| |||| |||||| ||||
Db   3310 CGCAATGATGAGACTCTACTATCAGTCCTGTGAGTGTGGCCGGTCATGTTCCGCCTCCATC 3369

Qy   2956 GCCAACTTCTCTGAGTTCTATGTGAGGCTCGAGGCGCAAACAATGAGGGTGTCGAGTGCCTG 3015
          ||||| ||||| |||| | |||| |||| |||| |||||| | |||||| |||||||||||
Db   3370 GCCAACTTCTCCCGAGTTCTACGTTGAGGCTCGAGGTGTGCCAACACGAGGGTGTCGAGTGCCTG 3429

Qy   3016 CGGCTGCTCAACGAGCATCATCGCTGGACTTTGATGAGATTATCAGGAGGCGGTTCCGG 3075
          ||||| ||||| ||||| |||| || |||||| |||| ||||||| ||| ||||||||
Db   3430 CGGCTACTCAATGAGGATCATCGGTGACCTTTGATGAGATCATCAGCGAGGATCGGTTCCGG 3489

Qy   3076 CAGTCGGAAAAGATCAAGACCATTGGTAGCACCTACATGGTGCCTCAGGCTGGCGAACGC 3135
          |||| ||| | |||||||| | | | || ||||| |||||| ||| | ||||| |||||
Db   3490 CAGTCGGAGCAGATCAAGACCTTGGCTGGCTTGGCTTGCTTCCCGCCGCCTCCGGCCTCAACGAC 3549

Qy   3136 AGCACCTACGATCAGTGGGCGCCGCTTCCAACATCACTGCCCTGGCTGACTACGCCATGCGG 3195
          || ||||| | ||| ||| ||| || || || |||| | |||| |||| |||||||| |
Db   3550 TCTACCTACGCAAGGGTGGGCAAGACCCACATCAAGGCACTGGCCGCGACTTTGCCATGAAG 3609

Qy   3196 CTCATGGAGCAGATGAAGCAGCACATCAATGAGCACTCCTTCAACAATTCCAGATGAAGATT 3255
          || || | ||| ||| |||||||| |||||||| | | ||||| | |||| ||||| || |
Db   3610 CTGATGAGCCAGATGAAGCAGTACATCAATGAGCACTCCTTCAACAACTTCAGATGAAGATC 3669

Qy   3256 GGGCTGAACATGGCCCCAGTCGTCGTGGCAGGTGTCATCGGGTTCGGAAGCCACAGTATGAC 3315
          |||||| || |||||| | | | | ||| |||| | ||||| | |||| ||||| || |||
Db   3670 GGGCTCAACATCGGCCCCGTGTGTCCGGGTGATAGGGGCACGCACGGGCTCAGTACGAC 3729

Qy   3316 ATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGGGGTCCCCGACCGA 3375
          | |||||||||| | ||| |||| | || | ||| ||||||||||||| ||||||
Db   3730 ATCTGGGGCAATACCGGTGAACGTGGCCAGCCGCATGGACAGCACACCGTACCCGGACCGC 3789

Qy   3376 ATCCAGGTGACCACGGACGACCTGTACAGAGGTTCTAGCGGTTGCCAAGGCGTACCAGCTGGAGTGT 3435
          ||||||| ||| |||||| |||| || || |||| || ||||| ||||||| ||||||||||| ||
Db   3790 ATCCAGGTAGTCTACCTGGCCGTGGCTGCCTGCCAACGTGGCTGCAGGTGTCGATCCTTATCATGGC 3849

Qy   3436 CGAGGGGTGGTCAAGGTGAAGGCAAGGGCAAGGGGGAGATGGGGGGC 3495
          ||||| |||||||||||| ||| ||||| | ||||| ||| ||||
Db   3850 CGGGGGCCGGTCGTCAAGGTCGGTCAAGGGGTCGAGATGATGAAGGAGG 3909

Db 1508 |||||| |||||| |||| |||||| ||||||||| ||| |||||||||
          CTCCATTGGACACAATCCGCCTCACTGGGGAGCTGAGCGCCCCTTCTACAACCACTTGGG 1567

Qy 1774 -CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGGATGATTCCAGCAAAGACAA 1832

Db 1568 TGGCAACCAGGTGTCAGCGGCGTGTTGCTGGCCTTGAGGAGGATGGGCTTTGAGGACCCCA------AGGA 1621

Qy 1833 CCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGGATGAGTTCCTGAGCCGTGC 1892

Db 1622 CAAGAATGCCCAGGAAAGTGCCAACCCTGAGGATGAAGTGACGAGTTTCTGGGTGTCGAGC 1681

Qy 1893 CATGCGATGCCGCAGCATTGATCAGCTGCGGGAAGGACCATGTGCGCCGGTTCTGCTCAC 1952

Db 1682 CATCGATGCCGCAGGAGTATTGACAGACTGCGAATCCGAACACGTCCGAAAGTTCCTCTTGAC 1741

Qy 1953 CTTCCAGAGAGAGGATCTTGAGAAGAAGAGTACTCCCGGAAGGTGGATCCCCGGCTTCCGAGC 2012

Db 1742 CTTTAGGGAGGCCCGACTTAGGAGAAGAAGTACTCCAAGCAGGTGGATGACCGATTTGGTGC 1801

Qy 2013 CTACGTTGCCTGTGCCCGTGGTCTTCTGCTTCATCGTGTTCCAGCTTCTCATCTT 2072

Db 1802 CTATGTGGGCTGTGCCCGCGTGTTTCTCCTTCATCGTGTTTGTCCAGATCACCATTGT 1861

Qy 2073 CCCACACTCCACCCTGATGCTTGGGATCATGCCAGCAGCGTCCTGCTGCTCGCTGCTAATCAC 2132

Db 1862 GCCCCACTCCTGTTCATGCTGAGCTTCTCCGTGGTTCCGTACTCGGCCTTGGT 1921

Qy 2133 CGTGCTGATCTGTGCTGGTGTACTCCGTGGTTCTCGTGGTTCCCTAAGGCCCTGCAACGTCT 2192

Db 1922 GGTGTTTATATCTGTGATCTGCCGTGTTGTGAAGCTCTTCCCTACTCCCCTGAGACACT 1981

Qy 2193 GTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGGCAGTTGGCATCTTTTCCGTCCT 2252

Db 1982 CTCCAGGAAGATAGTGCGGATCAAGAAGAACAGCACCCTGGTCGGGGTGTTCACCATCAC 2041

Qy 2253 GCTTGTGTTTACTTCTGCCATTGCCAATGTTTGCCCGGTTTGACAAGCTGGC 2312

Db 2042 CCTGGTGTTCCTCTCGGCTTTTGTTCAACATGTTCATGTGCAACTCTAAGAACCTGGTGGG 2101

Qy 2313 CTGTGCAGCCGCCGGATGCTGAATTTAACACCTGCTGCACATCGACATGCCTGCAGCA 2372

Db 2102 TTGGCTGGCAGAGAGCACAACATCACGTGACCAGGTGACATGTCATGTGATGGA 2161

Qy 2373 G------CTCAATTACTCTCTGGGCCTGATGCTCCCCTGTGTGAGGGCACCATGCCCAC 2426

Db 2162 GTCGGCCTTCAACTACACAGCCTGGGCGACGAGCAGGGCTTCTGTGTGGCAGCCCCAGTCCAA 2221

Qy 2427 CTGCAGCTTTCCTGCAGTACTTCATCGGGAACACATGCCGCGTGGGCAT 2486

Db 2222 CTGCAACTTCCCAGAGTACTTCACCTACAGCGGGACCTCCCAGTGCCTGGCTGCTGCCGT 2281

Qy 2487 CTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGCCTCATCTA 2546

Db 2282 GTTCCTGCAGATCAGCTGCATCGGGAAGGAAGCTGGTGCTGGCCATCGAGCTCATCTA 2341

Qy 2547 TTTGGTGCTGCTTCTGCTGTGGGTCCCCCAGCCACCATCTTTGACAACTATGACCTACTGCT 2606

Db 2342 ---CGTGCTCATCGGAGTGCCCGGTTGTCACACTCTTTGACAACGCTGACCTTCTGGT 2398

Qy 2607 TGGCGTCATGGCGTTGGCTTCTTCCAATGAGACCTTTGAATGAGTGCCTCCAGCTGC 2666

Db 2399 CACCGGCCAATGCCATAG---ACTTCAGCAACAACACGGGACCTCCCAGTGCCCTGAGCATGC 2455

Qy 2667 AGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGTGTTTGCGCTGGCGCT 2726

Db 2456 GACCAAGGTGGCCGCTGAAGGTGGTGACGCCTGTGTCATCATCATCTGTCTGCTGCTCT 2515

Qy 2727 GTATCTGACATGCTCAGCAGGTGGAGTCGAGCTGCTCCTGGAAACTACA 2786

Db 2516 GTATCTGCATGCTCAGCAGGTGGAATCCAGTGGAATCCTGTGACTTCCTCTGGAAACTGCA 2575

Qy 2787 GGCAACAGGGAGGAGAAGGAGATGGAGAGCTACACAACCGGAGGCGTGCTGCA 2846

Qy 645   GCTGGGGCATCCTGCGGCCAGTGCAGGTCGGGGGCGCGCTCTCGAGCAGGACCCGGCAGCCC 704

Db 428   CATTGCCAGTGGTGCTGCCCGTGCCCAGGTAGTGGCCGTGTTGCTGGCCCACAGCCAGCGC 487

Qy 705   CTCTGCGGGCCCTGTGTGTCCCTGTGTTCTTTGTCTACATCGCCTACACGCTCTCCCCAT 764

Db 488   CTCCGAGGGCATCGGTGACCGTGTCTTCATCTATACCATCTACACCCTGCCTGCCTGT 547

Qy 765   CCGATGCGGGCTGCCGTCCTCAGCGGCCTCTGGGCCTTGCATTGATCTTGC 824

Db 548   GCGCATGAGGGCTGCCGGCTGCTCAGCGGGTGCTTCTGTCGCCTCCACTTGGCCATCTC 607

Qy 825   CTGGCAACTTAACCTGGTGATGCCTTCCTCTGGAAGCAGCTGGGTGCCAATGCTGCT 884

Db 608   TCTGCACACCAGCCCCAGTTTCTGCTGAAACAGCTTGTCTCCAACGTCCCTCAT 667

Qy 885   GTTCCTCTGCACCAACGTCATTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCG 944

Db 668   CTTCTCTTGCACCAACATCGTGGGTGTGTGCACTCACTACCCGACGCGAGGTCTCCCAGAG 727

Qy 945   CCAGGCCCTTTCAGGAGACCCGCGGTTACATCCAGGCCCGCTCCACCTGCCTGCAGCATGAGAA 1004

Db 728   ACAAGCCTTCCAGGAGACCCGGGAGTGCATCCAAGCTCGGCTCCACAGCCGGGAGAA 787

Qy 1005 TCGGCAGCAGGAGCGGCGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAA 1064

Db 788   CCAGCAACAGGAGGCGCTCTCCGCTGTCTGTCGTCTCTCCCCGTCATGTTGCCATGGGAGATGAA 847

Qy 1065 AGAAGACATCAACACACAAAAAAAGGAACATGATGTTCCACAAGATCTACATACAGAAGCA 1124

Db 848   AGCAGACATCAACGCCAAACAGAGGATATGATGTTCCACAAGATTTACATCCAGAAACA 907

Qy 1125 TGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGGCTTCACCGGCTGGCATCCCAGTG 1184

Db 908   TGACAATGTGAGCATCCTGTTTGCTGACATCGAAGGCTTCACTAGCCTGGCATCCCAGTG 967

Qy 1185 CACTGCGCAGGAGCGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGC 1244

Db 968   TACTGCCCAGAACTGGTCATGCAGCCTCAACGAGCTCTTCGCCCGCTTTGACAAGTTGGC 1027

Qy 1245 TGGCGGAGAATCACTGCCTGAGGATCAAAGATCTTGGGGGACTGGTTACTACTGTGTGTCAGG 1304

Db 1028 TGCGGAGAATCACTGCTTACGGATTAAGATCCTCGGGGATTGTTACTACTGTGTCTCGGG 1087

Qy 1305 GCTGCGGGAGGCCCGGGGCCGACTGCCGGCCGCACCATGCCGCCGTGTGTGGAGATGGGGTAGACATGAT 1364

Db 1088 GCTGCCTGAAGCCAGAGCTGACCACGGCGCCGGCCAGGCTGACACTGGAGAAGCTGCGAGAGGAATGGGACATGAT 1147

Qy 1365 TGAGGCCATCTCGTGCTACTGGTGAGGTGACAGTGTGAAATGCGCGTGGGGCAT 1424

Db 1148 CGAGGGCCATCTCGTCGGTGCTGGAGGTGACAGGGTGACAGCGTGTGGGAAT 1207

Qy 1425 CCACAGCGGCGCGGCCGTCGCACTGCGCCGTCCTTGGCTTGCCGCAGTTCGATGTGTG 1484

Db 1208 TCACAGCGGGGAGAGTACACTGCCGTGTCCTTGGCCTTGCCAGAAGTGGCAATTCGACGTGTG 1267

Qy 1485 GTCCAATGATGTGACCCTGGCACTGGCCGCAGGAGGCCGGCATCCA 1544

Db 1268 GTCTAACGATGTCACACTGGCCAACCATGGCCAACCATGGAAGCTGGCGCGGCCAAGGCCAGGCCGCATCCA 1327

Qy 1545 CATCACTCGGGCAACACTCCAGTACCTGAACGGGACTACGAGGTGAGGCCGTGG 1604

Db 1328 CATCACCAAGGCCACCACTCAACTACCTGAACGCGGGACTACTGAGGTGAGGCTGTGTGG 1387

Qy 1605 TGGCGAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGGGC 1664

Db 1388 TGGTGAGCGCAATGCCGGTCAGGAGCACAGCAGCAGACACCTTCCTCATCCTCGCGCTG 1447

Qy 1665 CAGCCAGAAACGGAAAGACGGAGAAGGAGAGGGAGAGGAGCCATGCGCCAAGCTGGCCAAGCTCGGGGGCAA 1724

Db 1448 TACCCAGAAGCCGAAAAGATGAAGAAGAGAGAAGACCGCCAAGATGCGACCCAGAGAACCAA 1507

Qy 1725 CTCCATGGGAAGGGCTGATGCCCGCGCTGGGTTCCGATCGTGCCTTTCTCC-------- 1773

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Db  2576 GGCCACAGAGAAGAGAAGGAGGAGGAGCTGCAGGCCTACAACCGGCCGCCTTGCTGCA 2635
              ||||||||||||||||| |||| |||||||||
Qy  2847 TAACATTCTGCCCAAGGACGTGGCCGCCCACTTCCTGGCCCCGGGAGCGCCGCAATGATGA 2906
              ||||||||||||||||| |||||||||
Db  2636 CAACATTCTGCCCAAGGACGTGGCTGCCCACTTCCTGGCCCCGGGAGCGGCGCAATGATGA 2695

Qy  2907 ACTCTACTATCAGTCGTGTGAGTGTGGCTGTTATGTTTGCCTCCATTGCCAACTTCTC 2966
              ||| |||||||| || ||||||||||||| |||||||||
Db  2696 ACTGTACTACCAATCCTGCGAGTGCGTGGCTGTCATGTTTGCCTCCATCGCCAACTTCTC 2755

Qy  2967 TGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGTCGAGTGCCTGCGGCTGCTCAA 3026
              ||||||||||||||| |||||| |||||||||
Db  2756 CGAATTCTACGTGGAGCTAGAGGCCAACAATGAGGGCGTTGAATGCTACGGCTGCTCAA 2815

Qy  3027 CGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTCGAAAA 3086
              ||||||||||||||| ||||| ||||||||||
Db  2816 TGAGATCATCGCAGACTTTGATGAGATCATCAGTGAGGAGATCGGTTCAGGCAGCTCGAAAA 2875

Qy  3087 GATCAAGAACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGA 3146
              |||||||||||| ||||||| |||||||||
Db  2876 GATCAAGAACGACCATAGGTAGCACCTACATGGCTGCTCTCGGGCCTCAACGACTCCACCTATGA 2935

Qy  3147 TCAGTTGGCGGCCGCTCCACAATCACTGCCCTTGCTGACTACGCCATGCGCGGCTCATGGAGCA 3206
              ||||| ||||| |||||||||
Db  2936 CAAGGGCAGGCAAGACCCACACATCAAGGCTCTTCAGACTTCGCCATGCTGAAGCTGATGGACCA 2995

Qy  3207 GATGAAGACACATCAATGAGCACTCCTTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACAT 3266
              || || |||||||| |||||| |||||||||
Db  2996 AATGAAGTACATCAATGAGCACTCCTTCCTTCAACAACTTCCAGATGAAGATGAAGATCGGGCTTAACAT 3055

Qy  3267 GGGGCCCAGTCGTCGGGCAGGTGTCATCGGGCGTCGGAAGCCACAGTATGACATCTGGGGGAA 3326
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Db  3056 TGGGACCTGTAGTGCGGTCATTGGGGTCATTGGGTTGGGCTCGCAGCCTCAGTAGACATCTGGGGCCAA 3115

Qy  3327 CACAGTGAAATGTCTCTAGTGTATGACACAGCACGCAGGGGGTCCCGACCGGAATCCAGGTGAC 3386
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Db  3116 TACAGTAAAATGGCCAGCCGTGATGGACACTGGGGTGCCTGACCGCATCCAGTTAC 3175

Qy  3387 CACGGACCTGTACCAGGTTCTAGCTGCCAAGGGTCTACCAGCTGGAGTGTCGAGGGGTGGT 3446
              |||||| ||||||||||| |||||||||
Db  3176 TACAGATATGTACCAGGTGCTGGCCGCGCAACACATACCAGCTGGGAGTGCGGGGGTGTGGT 3235

Qy  3447 CAAGGTGAAGGGCAAGGGGAGATGACCACCTACTTCCTCAATGGGGGCCC 3497
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Db  3236 CAAGGTCAAGGGCCAAGGGGTGAGATGAGATGACCTACTTCCTCAATGGAGGGCC 3286
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                                                 PRIOR APPLICATION DATA:
                                                    APPLICATION NUMBER: US 60/005,498
                                                    FILING DATE: 04-OCT-1995
                                                 ATTORNEY/AGENT INFORMATION:
                                                    NAME: Highlander, Steven L.
                                                    REGISTRATION NUMBER: 37,642
                                                    REFERENCE/DOCKET NUMBER: UTSD:450
                                                 TELECOMUNICATION INFORMATION:
                                                    TELEPHONE:   (512) 418-3000
                                                    TELEFAX:     (512) 474-7577
                                                 INFORMATION FOR SEQ ID NO:  1:
                                                    SEQUENCE CHARACTERISTICS:
                                                    LENGTH: 3978 base pairs
                                                    TYPE: nucleic acid
                                                    STRANDEDNESS: single
                                                    TOPOLOGY: linear
                                                 US-08-726-214-1

                                                 Query Match           17.0%;    Score 604.4;  DB 3;   Length 3978;
                                                 Best Local Similarity  52.3%;    Pred. No. 7.2e-137;
                                                 Matches 1764; Conservative    0; Mismatches 1471; Indels 137; Gaps 14;
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Qy  153 GCCACCCAGCCCACCCCTGCGGCCCCCTCGGTGCCCCCTGGCAGGATGACGCCTTCAT 212
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Db   25 GCGCCCCGGCCGCTCGCCCGCGCCCGCCCGCGCCCGGGGCCTGCTGGTGGGCTGGGCGGCGAGGGGGCGGC 84

Qy  213 CCGGAGGGGGCGCCGCCCAGGCAAGGGCAAGGAGCTGGGCGGCGGCGGCGGGCCTT 272
             ||||||||||  |||||||||
Db   85 CCGCTGCATGGCGCTGGGATGGCGGCGGGCGGCGGCGGCGGCGGGGGGGGGGGGGGA 144

Qy  273 CGAGGATACCGGAGTGCAACGACAGCGGCGGCGCGAGGTGGGCCCGACGCGGT 332
             |||||||||| |||||||||
Db  145 GGCGGCGGCCGGGCGAGTCTGGGGGCGTCGGGTGCCCGAGCGGCGGCGGGCGGCGGGGGGGG 204

Qy  333 GCCCAGGAG------TGGGCGATCCTGCTGCGGCGGCCGTCGGTGCAGGTGTTCCAGTCGAAG 387
             ||||||||
Db  205 CTGCGGGGCGTGCGGATGAGGAGTTCGCGTGCCCCGAGCTGGAGCGCGTGTTCCGGCGGCTAC 264

Qy  388 CAGTTCCGTTCGGCCAAGCTGGAGGCCCTGAGGCCCTGTACCAGGAGGTGTACTTCTTCCAGATGAACCAG 447
             ||||||||||   |||||||||
Db  265 ACGCTGCGGCTGGAGAGCGGCGACGCTGAAGGCGCTGCGGCTCAGCGTGCTGCGCG 324

Qy  448 AGCAGCCTGCTGATGCGGTCGCTGCTCACAGCGGGTGCTGCTGGGCTTC 507
             |||||||||||||||||||
Db  325 GGCGGCCTGGCCTGGCCAGGCTGCTGGGCGCGCCGGGGCCCGCCGTGGCCTGGGCTAAG 384

Qy  508 CACGGCCGCACCCGGCCGCCGCGCCCTGCGCAGCCTGCCCTATGTGCGCCGGCTGGCCGCTGTTGGCGCACTGTTGGCGCACTGTTGGCACGGTCCGC 567
             ||||||||
Db  385 GGCTCGCACCCGTGCACTGCGCTCTTCCTGGCGGCTGCTCGTCGTGGTGTCGTGGTTCACCAACGTGCCGC 444

Qy  568 CTGTTCCTGGGGCTCATGGTGCTCATGGTGTGTGTGTAACCGGCA--------TAGCTTCCGCCAGGAC 618
             |||| ||||  ||||||| |||||||||
Db  445 TCGCTGCAGGTGCCCCAGCTGCAGCAGGTCGGCCAGCTCGGCCATCGGCGCTTCGGCGTGCTGTG 504

Qy  619 TCCATGTGGGTGGTGAGTTACGTGGTGCTGGGCATCCTGGCGCGCAGTGCAGGTCGGGGGC 678
             |||| |||||||||   |||||||||
Db  505 TTCGCTCGTGCTGTGCTGGTCCCTTCGCGCTGCCCGGCTGGCGCCGGTGCCGCGCCGGGGC- 563

Qy  679 GCTCTGCCAGCAGACCCGGCAGACCCCTGCGGGAGCCCCTCGCGGGCCTCTGTGTGCCCTGTGGTTCTTTGTC 738
             ||||||||||   |||||||||
Db  564 -----GGCAGCCGGTGCCGGCGACAGCCGATCAGGGAGGTCTGGCAGCTGTCCTTTGGTCACC 618

Qy  739 TACATCGCCTACACGGCTCCTCCCCATCCGCCATGCATGCGGCTGCCTGCCTCTCCTCAGCGGCCTGGGC 798
             |||| || |||||||||
Db  619 TTCGTGTCTCCATGCCCGCCTGCGCGCAGCCTGCGGCCATCGGCTTCGGCGCTGCGTG 678

Qy  799 CTCTCCACCTTGCATT---TGATCTTGGCCTGGCAACTTAACGTGGTGATGCTTCCTC 855
             |||||  ||| ||   |   ||  |||||||||
Db  679 GTGGCCCGCCTCGCACTTGCTCGTCACGGCTACGTTGGTCCCCGCAGCGCCCAAGCGTCTC 738

Qy  856 TGGAAGCAGCTCGGTGCCAATGTCGTGTTCCTCTGCACCAACGTCATTGGCATCTGC 915
             ||||  |||||||||
Db  739 TGGAGAACGCTGGGTGCCAACGCTCTGCTCTGCTCTCCTCCGTGTGAACGTGTATGCATCTTC 798
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RESULT 9
US-08-726-214-1
; Sequence 1, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
;   APPLICANT: Tang, Wei-Jen
;   APPLICANT: Gilman, Alfred G.
;   TITLE OF INVENTION:  SOLUBLE MAMMALIAN ADENYLYL CYCLASE
;   TITLE OF INVENTION:  AND USES THEREFOR
;   NUMBER OF SEQUENCES:  31
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Arnold, White & Durkee
;     STREET:  P.O. Box 4433
;     CITY:  Houston
;     STATE:  Texas
;     COUNTRY:  United States of America
;     ZIP:  77210
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/726,214
;     FILING DATE:  Concurrently Herewith
;     CLASSIFICATION:  435
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Qy   916 ACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGGACCCGCGGTTACATC  975
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Db   799 GTGAGGATCCTGGCTGAGCGCGCCCAGAGGAAGGCCTTCCTGCAGGGCCCGGAACTGCATT  858

Qy   976 CAGGCCCGGCTCACCTGCGATCCAGTGAGCATGAGAATCGGCAGCAGGAGCCGCTGCTGTCGGTA 1035
             |||  |||||| || |  |||||||||||||||  ||| |||| || ||||
Db   859 GAGGACCGGCTGAGGCTGAGGAGGATGAGAGAATGAGAAGGCAGGAGCCGCTGCTGCTGCTCAGGCCTC  918

Qy  1036 TTGCCCCAGCACGTTGCCATGGAGTAGAGCAATGAAGAGAGACATCAACAACAAAAAGAAGACATG 1095
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Db   919 CTGCCTCGGAATGTTGCCATGGAGGATGTGGAGGATGAAGGAGGACTT---CCTGAAGCCCCTGAGAGG  975

Qy  1096 ATGTTCCACAAGATCTACATACAGAGAAGCATGACAATGTCAGCATCCTGTTTGCAGACATT 1155
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Db   976 ATTTTCCACAAGATTTACATCCAGCGGCATGACAACGTGAGCATCTCTTTGCAGACATC 1035

Qy  1156 GAGGGCTTCACCAGCTGGATCCCAGTGCACTGCGCAGGAGGCTGGTCATGACCCTGAAT 1215
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Db  1036 GTGGGACTTCACAGGCTTGCGGCGTCACAGTGCCCCAGGAGCTGGTGGTGAAACTCCTCAAT 1095

Qy  1216 GAGCTCTTTGCCCGGTTGACAAGCTCGGCTGCGCAGGAATCACTGCCTGAGGATCAAGATC 1275
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Db  1096 GAGCTCTTCGGGAAGTTTGACGAGCTGGCCACAGAGAACCACTGCCGCCGCATCAAGGATC 1155

Qy  1276 TTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGAGGCTGCTGCGGACCCCAC 1335
             |||||| |||||||||||||| |  |   ||  ||| || |||||||| |||||||||||
Db  1156 CTGGGAGATTGCTACTACTGCGTGTCTGGGTGCTCCCTCAGCCCAAGACTGACCGCCCAC 1215

Qy  1336 TGCTGTGTGGAGATGGGGTAGCATGATTGAGGCTGTGTACGTGAGGTGACA 1395
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Db  1216 TGCTGTGTGTGGAGATGGGGTCGGCAGTCTCGGCTGCTGCGGAGGCCACT 1275

Qy  1396 GGTGTGATGTGAACATGCCGTGGGCATCCAGCGGCGGCGCGTCACGCGCGTCCTT 1455
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Db  1276 GAGGTGGACTTGAACATGCCTGTGGGGTCTGGCACCACCGGCAGGGTCTCTGCGGGGGTCCTG 1335

Qy  1456 GGCTTGGCGAAATGGCAGTTCGATGTGTGGTCCAATGATGTGGCTGACACCACATG 1515
             ||||| || || |||||| | |  | |||||| |||||||| ||||||||||||||
Db  1336 GGGCTCGCTGAGTTCGATGTGTGTCAGATCCTGCCAACCTGACCTGGCCAACGTCATG 1395

Qy  1516 GAGGCAGGAGGCCCGGGCTGCCTGCTGCTCGGGCGACTACTGCGGCAACACTCACTCGGGCAACACTCACTCGGGCAACTGA  1575
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Db  1396 GAGGCGGCTGCCGGCCTGCTGCTCGGGGCGACTGACTGTGCCAACATCCTGCCCAACCTGACCACCCTGGCCGTGTGAT 1455

Qy  1576 GGGGACTACGAGGTGGAGCAGCCAGGCCGTGTGGGCGAGCGCAAGCGTACCTCAAGGAGCAG 1635
             | |||||||  ||||||  || | |||||||| ||||| ||||  | ||||  ||
Db  1456 GGTGACTATGAGGTGGAGCAGCCGGGGCCGTGTGGGGTCTGGGGACGGAGAGATGTTGAAAACTCAT 1515

Qy  1636 CACATTGAGACTTTCTCATCCTGGGCGCAGCGCCAGGCAGCCAGGAAACGGAAAGAGGAGGCCATG 1695
             |||||||||||| |||  ||||| |||| | ||||||||||||  |||| ||||||||||||||||
Db  1516 AACATTGAGACCTTTTATTGTGCCCTC------GCATCGGGACAGCGGGAAAGATATTTCCAGGG 1569

Qy  1696 CTGCCAAGCTGCAGCGAGCGGACTCGGGCAACTCCATGATGCCGCGCTGGGTT 1755
             |||  ||||||||| ||||| |  ||| ||  |  || | || | |||||||||
Db  1570 CTGATTCTCTCAGACATAAAACCGGCCAGCAAGAGGATGAAGTTCAAGACCGTGTGCTACCTG 1629

Qy  1756 CCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCCTTCCCGCCAGATGGGCATTGAT 1815
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Db  1630 CTGTGCAGCTCATGGAGGTGGAGACACTGCACTGCCGGGAGATGTTCAAGGCCGAGATCCTTCTCCA  1684

Qy  1816 GATTCCAGAAAGACAACACCGGGGCACCCGGACACCATCTGAACCCTGAGGATGGAT 1875
             |||||| || ||| ||||  |||||||||||||||| |||  |||||| |||||||||
Db  1685 ----------------------------------------ACGTCATGACCTGTGAGGATGACGACACAG 1713

Qy  1876 GAGTTCCTGAGCCTGCCATGCGTGCCGCGAGCCGCAGGACCATGTG 1935
             ||||||||| | | ||| || |  | |||  |||||| || |
Db  1714 CGG----AGGGCACTGAGAACAGCCTCGGAAAAACTCAGAAAACCGCTCTTTTCTCTTAC 1769

Qy  1936 CGCCGGTTTCGTCGCTCACCTTCGCTCAACAGTGTCAACCACCACCCCCGCCCCTCCTGA 1995
             ||||  ||| |||   ||||||||| | |||||| | ||||||||||| |||||  | |||
Db  1770 AAACGTGTCCAAACCACCACCCCCGCCACACGTGTCAACGGCCACATCGGCCGCGCCTCCTGA 1829
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Qy  1996 GATCCCCGCTCACGTTGCCTGCTGCCCGTGTGGTCTTCGCTTCATCTGCTTC 2055
             ||||| |||||||||||| |||||| |  |----|||||||| ||||||||||
Db  1830 AGCCGCCAGATGGCTGAGCATGGCAGAGAC-----TGAACTTCTTCACCCTGAAGTAC 1884

Qy  2056 ATCCAGCTTCTCATCTTCCACCACTCCACCCCTGATGCTTGGGATCTGCAGCATCTTC 2115
             | ||| ||| |||||||  |||| ||| ||||| || |||||||| ||||||| |||
Db  1885 AAGCAAGCTGAGGAGGCGAAGTACCACCAGCTTCAGCGAGCTTCACCAGCGCGC 1944

Qy  2116 CTGCTGCTGTAATCACCGTGCTGATCTGTCGTGTGCTGTTATTCGGCCGCCTTGTACTCCTGGTTCTGTGTTCCCCT 2175
             || || |||| ||||||| |  |||| |||||| ||||  |||| | ||||| |||  |  |  |||||| |
Db  1945 GTGGTTCTGGCTCTCATTCTGGCCTCTGCCTTGTCACCTTGTCTTGCTCTACCTTGCTCTAATAATCCCA 2004

Qy  2176 AAGGCCCTGCCAACGTCTGTCTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTT 2235
             |||   ||||| |||| |  ||||| |  |||| |||||| || |||| |||| ||||||
Db  2005 CAGAGTGTGGCTGGTTGCTGTCTTCTGCTTGCTCGGTGTTCCTCGTGGCTTCCTGTGTC 2064

Qy  2236 GGCATCTTTTCCGTCCTGCTGTGTTGTTACTTCTGCGAATTTAAACATCACT 2295
             ||||||||||| ||| |||||||| || |||||||| | ||| | ||||||||
Db  2065 CTGTACCTACACATCACCCGGGT--------------CCAGTGTTTCCAGGTGCCTGACCA 2113

Qy  2296 CACACCCCATACGGAGCTGCAGCCCGATGCTGAATTTAAACACTCGTGAATTTAAAACCTGAGATC 2355
             |||  ||| |||||| |||||| |  | | ||  ||||||  ||||  | || ||||||||||||
Db  2114 TCCAGATCCGCACCGTCTTGTGCATCTTCATCGTGGTCTTAATCTACTGTGGCCCAAG 2173

Qy  2356 GCCTGCCACCTGCAGCTCAATTACTTCTCTCGGCCTGCTCCCCTGTGTGAGGGC 2415
             ||||  ||| | || | ||  |||| ||||||||| |||||||  ||||| ||||
Db  2174 GC--------TGTGGTGGCTGCCTCTGCCTGCTGGGCTCCAGTGCCCAACGGGT 2224

Qy  2416 ACCATGCCCACCTGCGAGCTTCCTGAGTACTTCATCGGGAACATGCTGCTGAGTCTTG 2475
             |||| ||   | || ||||| |||| || || || |||| ||| | |  |||||| |||
Db  2225 CCCTGGTGTCCTGTCCTTCGCTCGGGGCCGGGACACTGCTGCCTG-TCCCGCCCTGCGAG 2283

Qy  2476 GCCAGCTCTGTCTGTTCCTGGACCATCAGCAGATCATGCAGCAAGTGGCCATGATCTTTGTCTTG 2535
             |||| || |||||| | |||||| |||| ||  |||||  ||||||||||  | | |||||||  ||
Db  2284 TCTGCGGCCCCGTGCGGGCCTGTGTGGGCCTGCGGGCACCCTCGTCGGCGCTGCCCGCCATATTCCTG 2343

Qy  2536 GGGCTCATCTATTTGGTGCTGCTTCTCTGGGGTGCCCCACCACCATCTTTGACAACTAT 2595
             |||| |||| ||  | |||| | | | ||| | ||| | |||||||| ||||| |||||
Db  2344 CGGGGTCTCCTGCGTGCTCGCCGTGATCCTGTCACTACATCCTCAGT 2403

Qy  2596 GACTTACTGCTTGGGCGTTGGCGTTCTTCTCCAATGAGACCTTTGATGGGCTGGAC 2655
             | ||  ||| |  ||||||||||||  | |||| |||---------------
Db  2404 GTCCTGGAGCTCAGCG----------------------------GGTACGAAGGCC 2433

Qy  2656 TGTCCAGCTGCAGGGAGGTTGGCCCTCAAATATGACCCCTGTGATTCTGCGTGTGTTT 2715
             ||| || |||||| |||| |||| ||| ||| |||| |||||| |||| | || ||| |
Db  2434 ATGGGGGCCGGTGCCATCTCGGACGTGCAGCTTCGAGCCGATCATGGCCATCCTGCTATTC 2493

Qy  2716 GGCTGGCGCTGTATCTGCATGCTCCAGCAGTGAGTCGACTGCGCCGCCTAGACTTCCTC 2775
             |||||| || |  | | || || || ||||| ||| |||| || |  | ||||| ||||||
Db  2494 TCGTTGCACGGCTGGGCCTGCGCCGCGGTGATGTCAAGTGTGTCAGGTGGACTACCTC 2553

Qy  2776 TGGAAACTACAGGCAACAGGGGAGAAGGAGAAGGAGAGTGGAGAGTGGAGATGGAGATGGACATCACCGG 2835
             |||| | |||||||| | |||||| ||  |||||  ||  || ||| |  |||||||| |||||||
Db  2554 TGGGGCGGCCCAGGCCAGGCGGAGGAGGCGGGATGAAGATGGACGGCCCCGGAGCGC 2613

Qy  2836 AGGCTGCTGCATAACACATTCTGCCCAGAACGACTCTGGCGGCGGGAGCGC 2895
             |||||||| | ||| | || | | |  | |||| ||  ||  | ||||| |||
Db  2614 AGGATTCTCTTCAACCTCCTGCCAGCACTTCCTAAGTGTCCAACCCT 2673

Qy  2896 CGCAATGATGAACTTCTACTATCAGTCGTGTGAGTGTCGTGGCTCCCATT 2955
             || ||||| ||||| ||||||  |||| |||||  | || | |||| ||||
Db  2674 CGCAACATGGACCTGTTATTACCAGTCATATCGCTCTACATCTCGACGGTGGCCATCATC 2733

Qy  2956 GCCAACTTCTCTGAGTTCTATGTGAGCTGGAGCCGAAGGACCATGTG 3015
             || || ||||| | | || || || |||||||| |||| |||| ||||
Db  2734 CCCAACTTCAATGACTTTGATGAGCTGTCATGAGCAACTGGGAATGCTA 2793

Qy  3016 CGGCTGCTCAACGAAGAGATCATCGACTTTGATAATCAGGCAGGCGGTTCCGG 3075
             ||| ||||| ||  ||||| || |||| ||||| ||| || |  |||||| |
Db  2794 CGCCTTTCTCGAATGAGATCATCTGACTTTGATGAGCTCATGGACAAAGACTTTTTACAAG 2853

Qy  3076 CAGCTGGAAAAGAATCAAGAACGATTGGTAGCACCTACATGGCTACACGCCTGAACGCC 3135
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Db  2854 GACCTTAGAGAGATCAAGACCATTGGGACGACGTACATGGCTGCTGTGTGGGCTGGCGCCC 2913
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Qy   466 CTGCTGCTGGGCCTCGCTTCCCGGGAGCAGCAGCGCACTCGAGCGCTGGACGCGCTCCCTGTCC 525

Db  3136 --------AGCACCTACGATCAGGTGGGCCGCTCCCACATCACTGCCCCTGCCTGACTAC 3186
                     ||||   |||  ||| ||||||||| |||||||||||  ||||||
Qy   637 TACGTGGTGCTGGGCATCCTGGCGCTGCGCGGTCGGGGCGGCCTCTCGCAGCAGACCCG 696

Db  2914 ACTGCTGGGACCAAGGCTAAGAAGTCGCATCTCCTCCCACCTCCTCAGCCGTTGGCAGATTTT 2973
          |  ||   ||||||   ||||||||  |||||||| ||||||| |||| |||| |||||||
Qy   526 GGCTTGGTATGGGTCGCGCGCTCTAGCGCTGCTGCCAGCTAGCCATCGGGCGGGGCGGTG 585

Db  3187 GCCATGCGGCTCATGGAGCAGATGAAGCACTCCTTCAACAATTCCAG 3246
          |||  ||||| ||| ||||| ||| |||||||   |||| |||||||
Qy   697 CGCAGCCCCTCTGGCGGCCCTCTGGTGCCCGTGTTCTTGTCTACATCGCCTACACGCTC 756

Db  2974 GCCATCGAGATGTTTGATGTCCTGGATGAGATCAACTACCAGTCTTATAACGACTTTGTG 3033
          |  ||||    || |||| | ||||||||||  ||||||| ||  ||||| || ||||
Qy   586 GTGAGCGGCCTGGACCAGGTGTCCATGGCCCTGGCCCTCTCCAGCGGCGGCGGTCATG 645

Db  3247 ATGAAGATTGGGCTGAACATGGGCCCAGTCGCTGCGCAGGTGTCATCGGGGCTCGGAAGCCA 3306
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Qy   757 CTCCCCATCGATCGGGCTGCGCCGTCCTCCAGCGCGGCTGGGCCTCTCCAACCTTGCATTTG 816

Db  3034 CTCCGTGTTGGGCATCAATGTTGGCCCCGTGGCTGGAGTGATCGGGGCTCGCGATCTG 3093
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Qy   646 CTGCCCTTGGGCATGCGGGACGCCCGTCCGCGGGGCTCGCGGGGCTCGCGATCTG 705

Db  3307 CAGTATGACATCTGGGGAACACAGTGAATGTCTTCAGTCGTATGACAGCACGGGGGTC 3366
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Qy   817 AT--------CTTGGCCTGCAACTTAACCGTGGTGATGCCTTCCTCTG--GAAGCAG 864

Db  3094 CAGTATGACATTTGGGGAACACACGTCAATGTGGCCAGTCGGATGACAGTACCGGCGTC 3153
          ||||||||||| |||||||||||| || |||||||||| ||||||||  |||||||
Qy   706 CTGGTCTCCGGCTGTATCTTGGGCCACAGCGGCCTGCCCACTGCTGCCGCAG 765

Db  3367 CCGACCGAATCCAGTGACCACGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAG 3426
          |||| |||||||| ||||| ||||| ||||||||| ||  |||||| |||||||||
Qy   865 CTCGGTGCCAATGTGCTGCTTCCTCTGCACCAAGTCATTGGCATCTGCACCACACTAT 924

Db  3154 CAGGGCAGGATCCAGGTTCACAGAGAAGTTCACCGGCGTTCCTTACCGGC 3213
          ||||| ||||| |||||| |||  ||||  |||| |||||||| |||||
Qy   766 TTGGGCAGCAAACGCAGTGCGTTGCCTGTGCCGCGGCGGGGAAGTTACCACAAGGCG 825

Db  3427 CTGGAGTGTCGAGGGGTGGTCAAGGTGAAGGTGAGGGGAGATGACCACCTACTTCCTC 3486
          |||||||||| ||||||| |||  |||||||| |||||  |||| |||||  ||||||
Qy   925 CCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGACACCCGGGTTACATCAGCCCCGG 984

Db  3214 TTCGTGTGCCGAGGCAAAGTCAGTGTCAGTGTGCCGCGGCCAAGGTGAGATGCTGACATACTTCCTG 3273
          |||||||| ||||| |||  ||||| |||||  |||| |||||||||  ||||||||||
Qy   826 CTGATGGAGCGGCGCCCTGCGGGCCCACGTTCCGGGAGGCACTCAGCTCCCTGCACTCACGC 885

Db  3487 AATGGGGGCCCC 3498
          ||||||| |||
Qy   985 CTCCACCTGCAGCATGAGAATCGGCAGCAGGAAGAATCGAGCAGGAGCGGCTGCTGTGCTGTATTGCCCCAG 1044

Db  3274 GAAGGCAGGACC 3285
          |||| |||||
Qy   886 CGGCGGCTGCTGGACACCGAGAAGAAGAAGCAACCAAGACACACACTTCTCTTGTCATCCTTCCTGCC 945

Qy  1045 CACGTTGCCATGGAGATGAAAGAAGAACATCAACAACAAAAAAGAAGA----------- 1091
          |||  ||||| ||||||||||| |||| |||| |||||||||||||||
Db   946 TACTTCTGCCCCGAGAGATGAAGGCAGAGATCATTGGCACGGCTGCAGCAGGACAGGGGTCA 1005

Qy  1092 --------------------CATGATGTTCCACAAGATCTACATACACAGAAGCATGACAATGTCAGC 
          |||||| |||  |||||||||||||||||||||||
Db  1006 CGGGCAGAGAGCACTAACACAATTTCACAGCCTCATGTCATGCTCTGGCATCCCAGTGACACCAGGGAGTCAGC 1065

Qy  1138 ATCCTGTTTGCAGACATTGAGGGCTTCACCAGCTGACCTGCGCACTGCGCAGGAG 1197
          |||| ||| |||||||||||||| |||||| |  || ||||||||||||||||
Db  1066 GTGCTGTATGCTGACATCGTGGGCTTCACGCGGTCTGCCAGCGAGTGTTCCCTAAGGAG 1125

Qy  1198 CTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTGACAAGCTGGCTGCGCGAGAATCAC 1257
          ||||||  |||| |||  |||| |||||||| ||| |||| ||||||| |||||| ||
Db  1126 CTGGTGCTCATGTCTCAATGAGCTCTTTGCCCAAGTTCGACCCAGCATCGGCCAAGGAGCATGAA 1185

Qy  1258 TGCCTGAGGATCAAAGATCTTGGGGACTGTGTTACTACTGTGTGTCAGGGTGCCGCGGAGGCC 1317
          ||||||| |||||||||| |||||| ||||||||||||| ||||| ||||||||||||
Db  1186 TGCATGCGGATCAAGATCCTGGGGGACTGTTACTACTGTGTCTCTGGGCTGCCACTCTCA 1245

Qy  1318 CGGGCCGACCATGCCCACTGCGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCG 1377
          |||||  ||||||| |||||| || |||||||||  |||  |||||||||||||||
Db  1246 CTGCCAGACCATGCCATCAACTGCGTGCCGCGGTGGCCATGATGTGCCGGGCCATCAGG 1305

Qy  1378 CTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGCATCCACAGCGCGGCGC 1437
          ||||  |||||  |||||||| ||||| |||| |||||| |||||||||||||||||
Db  1306 AAACTGGGGCAGCCCACTGGGCTGTGGCATCAACATGCGTGTGGGGCCGTGCACTCAGGCAGC 1365

Qy  1438 GTGCACTGCGGCTGGGAATGCAGTTGGCAGTTCAAGAGTGGGTCCAATGATGTG 1497
          ||| ||||| |||||||  | ||| || ||||||| |  ||| ||||||||
Db  1366 GTACTGTGTGGAGTCATCGGGCTGCAGAAGTGGCAGTATCGGCGTTGGTCACATGATGTC 1425

Qy  1498 ACCCTGCCAACCACATGAGAGGCAGCAGAGGCCCGGCTGCCCATCCATCTCGGGCA 1557
          || |||| ||||||||| ||||| |||||| |||||| |||||||||||||||||
Db  1426 ACACTGCTAACCACCATGAGAGGCGGGGTTACCGGCGTGACATCATCACACAGGGGCT 1485

Qy  1558 ACACTCAGTACCTGAACGGACTACGAGGTGGAGCTGGCCGTGTGGGCGAGCGCAAC 1617
          |||||||||||||||||| |||||||||||| ||||||||||||| |||||
Db  1486 ACCCTGCCCTGGGCCACTGTGTGGGCGAGGGGCTTATGCTGTGGAGACGCAGGCATCGGGGAC 1545

Qy  1618 GCGTACCTCAGGAGCAGCAGCACATTGAGACTTTCCTCATCCTCTT 1677
          ||  |||||
Qy   577 GGGCTCATGGTGGTGTGTAACGGCATAGCTTCCGCCAGGACTCCCGGCAGGACTGGGTGGTGAGT 636
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RESULT 10
US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3518
; SOFTWARE: FastSEQ for Windows Version 3.0
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2

  Query Match        14.4%;   Score 512.4;   DB 4;   Length 3518;
  Best Local Similarity   49.8%;   Pred. No. 1.4e-114;
  Matches 1571;   Conservative   0;   Mismatches 1506;   Indels   75;   Gaps   8;
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Qy   409 GAGCGCCTGTACCAGCGGTACTTCTTCCAGATGAACCAGAGCAGCCTGACCTGCTGATG 468
          |||||| |||||||   ||||| |||| |||||  | ||  |||||||||||||||||
Db   286 GACCTCTTCTACGAGACCTACTACAGCCTGAGCCAGCAGCCCAGCAGTACCCGCTGCTCTG 345

Qy   469 GCGGTGCTGGTCTCGTGCTCGCTGCGCGCGCTGCTCGCGAGTGGCCAGCGGCAGG 528
          |||| |||||||||||||||||| || ||||||||| |||| |||  |||||||
Db   346 CTGGGGATCGTGCTCTGTGCCGGCCTCTGTCGTGTTGGCCTGTCCAGTCGGGCAGG 405

Qy   529 CAGCTTGCCTATG---------TGGCCACTGTTGGCCGTGCCTGCGCCCGCCGCCGTGTTCGTG 576
          |||| ||||| ||        ||| || ||  ||||||||||||||||||||||||||||
Db   406 GAGCTGACCTTCAGACCCGAGCTTCCTGACCACTGTCGTGCGCGCACTGTCTGTGGCGGCTTTCTCG 465

Qy   577 GGGCTCATGGTGGTGTGTAACGGCATAGCTTCCGCCAGGACTCCCGGCAGGACTGGGTGGTGAGT 636
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Db   1546 CCCTACCTTCGGGAGCTAGGGAGGCCTACCTATCTGGTCATCGATCCACGGGCAGAGAGAG 1605

Qy   1678 AAAGAGGAGAAGGCCATGCTGGCCAAGCTGGGCGACTGGGCCAACTTCATCGAAGGG     1737
          |||  |||||||| ||||
Db   1606 GAGGATGAGAAGGGCACTGCAGGAGGGCTTGCTGTCTCGCTTGAGGGGCCTCAAGCATGCGT 1665

Qy   1738 CTGATGCCCGCGCTGGGTTCCTGATCGTGCCTTCCCGGACCAAGGACTCCAAGGCCTTC   1797
          ||||||  | | |
Db   1666 CCATCACTGCTGATGACCGTTACCTGGAGTCCTGGGGGGCAGCCAAGGCTTTTGCCCAC    1725

Qy   1798 CGGCCAGATGGGCATTGATTGATGATTCCAGCAAAGACAACGGGGGCCACCCCAAGATGCCCTG--A 1855
          |||
Db   1726 CTGAGCCACGGAGACAGCCCTGTGTCCACCTCCACCCTCCCGGAGAAGACCCTGGCT         1785

Qy   1856 ACCCTGAGGATGAGGTGGA-TGAGTTCCTGAGCCCTGCCATCGATGCCCGCAGCATTGAT    1914
          |||||||       |||| |
Db   1786 TCCTTCAGCACCAGTGGACACCCCAAGATGCCGAGCCCGTACCCCCCGGGGACTAGATGATGAA 1845

Qy   1915 CAGCTGCGGAAGGACCCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAG      1974
          |||  |||
Db   1846 CTGACACCGGAGATGCCCAAGTTCTTCCAGGTCATTGAGCAGCTCAACTGCGCAGAAACAG   1905

Qy   1975 AAGAAGTACTCCCGGAAGGTGGATCCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTG   2034
          |||||||
Db   1906 TGGAAGCAGTGAGAGGACTTCAACCCACTGACACTGTACTTCAGAGAGGAAGGAGAGGTGAGG 1965

Qy   2035 GTCTTCTCGCTTCATCGTCTTCATCCAGCTTCTCATCTTCCCACACTCCCGTGATGCTT    2094
          |||||
Db   1966 AAAGAGTACCGACTCCTCTGCGACTTCCCGGCCTTCAAATATACTATGAAGCCTGCCACCTTCCTG 2025

Qy   2095 GGGATCTATGCCAGCATCTTCCTGCTGCGCTGCTAATCACCGTGCTGATCGTGCTGTGTAC   2154
          |||   ||||    ||||
Db   2026 GTTTTTCTCTCCAACTTCATCATCCAGATGCTAGTGACAAACAGGCCCCCCAGCTCTGGCC   2085

Qy   2155 TCCTGTGGTTCTCTCGTTCCCCTAAGGCCTGGTCAACGTCTGTCCCCGCAGCATTGTCCGCTCA 2214
          || ||          |    |||| ||
Db   2086 ATCAC---GTATAGCATCACTTTCCTCCTCTCCTTCCCCATCCTTTTGTCTGCTTCTCA      2142

Qy   2215 CGGGCACATAGCACCGCAGTTGACATCTTTTCCGCTCCTGCTGTGTTTTTACTTCCGCCATT  2274
          ||||
Db   2143 GAGAGACCTGATGAGGTGTGTCCTGAAAGGCCCCAAGATGCTGCACTGGGCCTGCCCACTG   2202

Qy   2275 GCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTGTGCGAGCCCGGATGCTGAAT   2334
          |||       ||||
Db   2203 TCTGGCCTTGGTGGCCACACGACCAGGACTGAGAATAGCCTTGGGCACCCACCATCCTC     2262

Qy   2335 TTAACACCTGCTGACATCACTACTGCCTGCCACCTGCCAGCTCAATTACTCTCTGGGCCTG   2394
          ||||
Db   2263 CTTGTCTTTGCCATGGCCATTACCAGCCTGTTCTTCCTTCTTCCCAACATCATCAGACTCAGAC 2322

Qy   2395 GATGCTCCCCTGTGTGAGGGCACCATGCCACCTGCCCAGCTTTCTGAGTACTTCATCGGG    2454
          ||||
Db   2323 TTCCAAGCTCCCAAATGTCCTCCATGATTTCCAACCTCTCCTGGGAGCTCTCCTACTTCCTGAA 2382

Qy   2455 AACATGCTGCTCTTGGGCCAGCTCTGCTCTTCCTGCACATCAGCAGCATCGGGAAG        2514
          ||||
Db   2383 CTGCCTCTCATCAGTGTCCCCATACTGCACTGCTGCACGCGTGGCTTCCTCTCCTGC        2442

Qy   2515 TTGGCCATGATCTTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCA    2574
          |||||| ||||   |||
Db   2443 TCCCTCTTTCTGCACAATGGCTTCGAGCTGGAAGCTGCTCGCTGCTGTGTGGCTGGCG     2502

Qy   2575 GCCACCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGCTTCGCCATGCTGTCTTCTTCCAAT 2634
          ||||
Db   2503 GCATCCTGCTCCCTTCCTTCCTGCACTCCAGGACTCCCATGCGTCCGGAATGCCATCGTCCGC 2562

Qy   2635 GAGACCTTTGATGGGCTGGACTGTCCAGCTGACTGCGCCCGAGGGAGGGTGGCCCTCAAATATATGACC 2694
          ||||||  ||||   |||
Db   2563 CTCTTATCTGGGCCCCTGGACTCCAGGCCCGGAGTGCTGAAGAGCCCAAACTGATGGGT   2622

Qy   2695 CCTGTGATTCGTCGTGTTGGCGTGGCGTCATGCTCAGCAGGTGGAGTCG               2754
          || |    |||||    |||| ||
Db   2623 GCTATCTCCTTCTTCATCTTCTTCTTCACCCTCCCTTGTCCTTCCTGGCTCGGCTCGCGGAATGAGTAC 2682
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Qy   2755 ACTGCCCGCCTAGACTTCCTCTGGAAACTACAGGCAACACGGGAGGAGGCAACGGAGGAGGAGATGGAG 2814
          |||||||  ||||||||
Db   2683 TACTGCCGCCTGGACTTCCTGTGGAAGAAGAAGAGCTGAGGCAGGAGGAGGAGGAGGAGGAGACAGAG   2742

Qy   2815 GAGCTACAGGCATACAACCGGAGACGGCTGCATAACATTCTGCCCAAGGACGTGGCGGCC   2874
          ||||  |      |||
Db   2743 ACGATGGAGAACCTGACTGGCTGTCTCTTGGAGACGGTGCTCCTCTGCACACGTGGCCCCCC    2802

Qy   2875 CACTTCCTGCCCCGGGAGGCCCGGCCCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTG 2934
          |||| ||  |     ||
Db   2803 CAGTTCATTGGCCAGAACCGGCCAACCGGGGGATCCTCCACCCCAGTCCTATGAATGCGTT   2862

Qy   2935 GCTGTTATGTTTGCCTCCAATTGCCAACTTCTCTGAGTTCTATGTGGAGTCCGAGGCCAAAC 2994
          || ||||
Db   2863 TGTGTCCTTCCTTCGCCTGCCCTCAGTCCCAGACTTCAAGGAGTTCTACTCTGAATCCAACATCAAT 2922

Qy   2995 AATGAGGGTGTCGAGTGCCGTGCCCGGCCGTGCTCAACGGAGTCATCGCTGCGATGGAGCAC 3054
          |||      ||||
Db   2923 CATGAGGGGCCTAGTAGTTGTGTCTGAGGCTGCTCAATGAGATAATTGTCTGATTTTGATGAGCTG 2982

Qy   3055 ATCAGCGAGGAGCGCGGTTCCGGCAGCTGGAAAAAGATCAAGACGATTGGTAGCACCTACATG 3114
          ||||  | ||||||
Db   2983 CTCTTCCAAGCCCAAGTTCAGTGGGGTGGAGAAGAGGATCAAGACCATCGGCAGCACCTACATG 3042

Qy   3115 GTCTTCTCGCTTCATCGTCTTCATCCAGCTGCTGGGCTGAACGGCCAGCAC-------CTACGATCAGTGGGC 3156
          | |||  ||
Db   3043 GCAGCCACAGGCTTAAATGCCACCTCTGGACAGGATGCACAACAGGATGCTGAACGGAGC 3102

Qy   3157 CGCTCCCACATCACTGCCCTGCGCTGATCGTGTGATCGTCGGCTGATGGGCGATGAAGCAC 3216
          ||   || ||||
Db   3103 TGCAGCCACCTTGGCACTATGGTGAAATTTGCCGGCCCTGGGGTCTCTAAGCTGACGTC     3162

Qy   3217 ATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGACATGGGCCCCAGTC   3276
          |||||  ||| ||||||
Db   3163 ATCAACAAGCATTCATTCAACAACTTCCGCCTGCCGGAGTGGGGTTGAACCATGACCCCGTA 3222

Qy   3277 GTGGCAGGTGTCATCGGGGCTGCGAAGCCACAGTATGACACATGACACAGTGAAT         3336
          ||||        ||||||
Db   3223 GTAGCTGGAGTTATTGGGCCCCCAGAAGATGCCGCAATATGACATTTGGGGCACACAGTGAAC 3282

Qy   3337 GTCTCTAGTCGTATGGACAGCACGGGGTCCCGACCGGGGTGTGCGAATCCAGGTGACCACCGACCTG 3396
          ||  | |||||
Db   3283 GTGGCCAGCCCGCATGGAGGTACAGGAGTCCTTGCAAAATCCAAGTGACTGAGGAGACA      3342

Qy   3397 TACCAGGTTCTAGCTGCCAAGGGTACCAAGTGTGCTACCAGTCCCACACCTGTCATCATCTCAAGGTGAAG 3456
          |||
Db   3343 GCATGGCCCTACCAGTCCCTGGGCTACCTACACCTGTCACCCTCACTTCCTGAA            3402

Qy   3457 GGCAAGGGGGAGATGACCACCTACTTCCTCAA 3488

Db   3403 GGCAAAGGGCAGCTCTGCACCTACTTCCTGAA 3434
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;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/726,214
;    FILING DATE:  Concurrently Herewith
;    CLASSIFICATION:  435
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 60/005,498
;    FILING DATE:  04-OCT-1995
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Highlander, Steven L.
;    REGISTRATION NUMBER:  37,642
;    REFERENCE/DOCKET NUMBER:  UTSD:450
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (512) 418-3000
;    TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO: 15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4601 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-726-214-15
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Query Match   13.7%;   Score 485.2; DB 3;   Length 4601;
Best Local Similarity 52.2%;   Pred. No. 6.6e-108;
Matches 1458; Conservative 0; Mismatches 1178; Indels 156; Gaps 11;

US-08-307-896-5
; Sequence 5, Application US/08307896C
; Patent No. 6034071
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Srinivas Ravi
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
; FILE REFERENCE: 29770
; CURRENT APPLICATION NUMBER: US/08/307,896C
; CURRENT FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 4008
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-08-307-896-5

Query Match   12.9%;   Score 458.6; DB 3;   Length 4008;
Best Local Similarity   50.1%;   Pred. No. 1.8e-101;
Matches 1346; Conservative   0; Mismatches 1279; Indels 60; Gaps 6;

Qy	852	CCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTCCTCTGCACCAACGTCATTGGCAT	911
Db	624	CCTGTTCTGCAGATACTGCCAATGTGATCATTTCATTTGTGGGAACTTGGCGGGAGC	683
Qy	912	CTGCACACTATCCAGCAGAGGTGTCTCAGCCGCCAGGCCTTTCAGGAGACCCGCGGTTA	971
Db	684	CTACCACAAGCACCTCATCGAGCTTGCCTTGCAGCAAACCTATCGGGACACGTGTAATTG	743
Qy	972	CATCCAGGCCCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGCGGCTGCTGCTGTC	1031
Db	744	CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAACGGCAGCAGGAACGGCTCCTGCTCTC	803
Qy	1032	GGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGAAGAGAAGAACATCA----------A	1076
Db	804	CTTGCTGCCAGCTCACATCGCCATGGAGATGAAAGTGAAAATCATTCAGGAGGCTGCAGGG	863
Qy	1077	CACAAAAAAGAGAGAGATG---------ATGTTCCACAAGATCTACATACAGAAGCA	1124
Db	864	CCCCAAAGCAGGACAGATGAAGAACACAAACAACTTCCACAATCGTATGTCAAACGACA	923
Qy	1125	TGACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCTGCATCCCAGTG	1184
Db	924	CACCAAGTGAGCATGAGCATCATTACGGCTGACATTGTTGGCTTCACCCGGCTGCAAGCGATTG	983
Qy	1185	CACTGCGCAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGC	1244
Db	984	CTCCCCTGGCGAACTGGTCCACATGGTCCAATGCTGAATGAACTCTTTGGGAAGTTTGATCAAATAGC	1043
Qy	1245	TGCGGAGAATCACTGCCTGAGGATCAAGATCTTCGGGGACTGTGTTACTACGTGTGTCAGG	1304
Db	1044	AAAGGAGAATGAATGCATGAGAATTAAAATTTTAGGACGACTGCTATTACTGTGTTTCCGG	1103
Qy	1305	GCTGCGGAGGCCCGGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGAT	1364
Db	1104	GCTCCCTATATCACTCCCTAACCATGCCAAGAACTGTGTGAAAATGTGGGATTATGTG	1163
Qy	1365	TGAGGCCATCTCGCTGTGGTACGTGAGGTGACAGGTGACAGTGTGAATGTGAACATGCGGCGTGGGCAT	1424
Db	1164	CGAAGCCATAAAGAAAGTGAGGGATGCTACCGGAGTTGATATCAACATGCGTGTAGGAGT	1223
Qy	1425	CCACAGCCGGCGGCGTGCGACTGCGCGC	1484
Db	1224	GCAATTCTGGGAACGTTCTCTGTGTGATTGGTCTCCAGAAGTGGCAGTATGATGTGTG	1283
Qy	1485	GTCCAATGATGTGACCCTGGCCAACCACATGAGGAGGCCGCATCCA	1544
Db	1284	GTCTCATGATGTTACTCTGGCAACCACATGAGAAGCTGGAGAGCTCGGGCGTGTTCA	1343
Qy	1545	CATCACTCGGGCAACACTGCAGTACCTGAACGGGCATGGGG	1604
Db	1344	CATTTCTTCAGTCACTCTGAGCACTTGAATGGGGCTTATAAAGTGGAGAAGGAGATGG	1403

Db	3246	ACAGATATCTGCTCCTACCCCAGAGTACTTTGTCTTCACTGGGCGTGTTGGCCATGGTGACG	3305
Qy			
Db	2479	AGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGG	2538
Db	3306	TGTGCAGTATTTCTCCGGCTTAACTCTGTCCTGCTGCTGTGTCTGCTCATTATGATC	3365
Qy	2539	CTCATCTATTGGTGCTGCTTCTGCTGGTGGTCCCCAGCCACCATCTTTGACAACTATGAC	2598
Db	3366	GCCATCTACGCCCTGCTG----------------ACAGAGACCATCTAT---------	3398
Qy	2599	CTACTGCTTGGCCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTGATGGGCTGGACTGT	2658
Db	3399	---------GCAGGTCTCTTTCTGAGTTATGACAACCTGAACCAC	3434
Qy	2659	CCAGCTGCAGGGAGGGTGGCCCTCAAATATGACCCCGTGATTCTGCTGGTGTTTGCG	2718
Db	3435	AGTGGAGAGAGATTTTCTGGGGACCAAGGAGCATCACTGCTACTGATGTCTACTGTTCCTT	3494
Qy	2719	CTGGCGGCTTGTATCTGCATGTCACAGCAGTGGAGTCGAGTCGACTGCGCCCGCCTCCTCTGG	2778
Db	3495	CTTGCTGTGATTCTACCATGGACGACAGGGAGGAGGAGAATGAACACACCGGGTACAGTTCCTGTGG	3554
Qy	2779	AAACTACAGGCAACAGAGGGAGAGGAGGATGAAGAGACATACAACCGGAGG	2838
Db	3555	CGAGTACAGGCCAAAGAGGATCAACGAGATGAAGATGAGAGACTTGAGGAGGAACACAATGAGAAC	3614
Qy	2839	CTGCTGCGATAAACATTCTGCCCAAGGACGTTGGGCCGGCCACTTCCTGGCCCCGGGAGCGCCGGC	2898
Db	3615	ATGCTTCGCAATATCTTACCCGGACCACGTGGCCCCGCGTGGGCCCACTTCCTCCGGGAGAAGAGACAGAGAC	3674
Qy	2899	AATGATGAACTCTACTATCAGTCCGTGTGAGTGGCTGTGTGGGCTTATGTTTTGCCTCCATTGCC	2958
Db	3675	AATGAGGAGGCTGTGTATTCTCAATCCTATGATGCGGTTGCCTCTGTCTCCAGACTGTCCATTCCT	3734
Qy	2959	AACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGTCGAGTGCTGCTGCGG	3018
Db	3735	GGATTTGCAGACTTTTTACTTCCAGACAGACAGAAAATGAACACCAGGAGTGGAATGTCTCGGCGC	3794
Qy	3019	CTGCTCAACGAGGATCATCGCTGACTTGATGAGATTATCAGCGAGGAGGCGGTTCCGCGCAG	3078
Db	3795	TTGCTGAATGAAGATCATTGTGACTTTTGATGAGTTACTTGGAGAGGACACCGCTTTCAGGAC	3854
Qy	3079	CTGGAAAGATCAAGACGATTGGTACGACCTTACGGCTGCCTCAGGGCTGCTGAACGGCCAGC	3138
Db	3855	ATAGAGAAGAGATTAAGAACCATTGGTAGTAGTACATACGTGGTCTCTCAGACTGTCACCAGAG	3914
Qy	3139	ACCTACGA---TCAGGTGGGCCGCTCCCACAACTCTGCCCTGACACGGCCATGCGG	3195
Db	3915	AAACAGCAATGTGAAGATAAATGGGACATTTGTGTGCGCCTGGCTGACTTCTCTTTTGCC	3974
Qy	3196	CTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATT	3255
Db	3975	CTGACTGAAAGCATCACAGAGATACAACAGCATTCGTTCAACAATTTTGAACTCCGTATT	4034
Qy	3256	GGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGGCTGGAAGCCACAGTATGAC	3315
Db	4035	GGCATCAGCCATGGCCATGCCGTGTGCTAGCAGGTGTAATTGGCGTAAGGAAACCACCACTATGAC	4094
Qy	3316	ATCTGGGGGAAACAGTGAATGTCTGTAGTCGTATGGAGCAGCACGGGGGTCCCGACCGA	3375
Db	4095	ATTTGGGGTAAAACTGTGAACTTGCAAGCCGAATGGACAGCACAGAGTGAGTGGCGCCGG	4154
Qy	3376	ATCCAGGTTGACCACCGACCTGTACCAGGTTCAGCTGCCAAGGGCTACCAGCTGGAGTGT	3435
Db	4155	ATCCAAGTTCCTGGAGGACCTATCTCATCCTGAAGGATCAGGGGCTTTGCCTTCGACTAC	4214
Qy	3436	CGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGA	3467
Db	4215	CGGGGGAGAGATATATGTGAAGGGGCATCACGCGA	4246

RESULT 12

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Qy  2682 CAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGCGCTGTATCTGCATGCTCA 2741
         ||||  |||| ||| |||  |||| ||| |||||  | | |  || | || ||||
Db  2472 GAAGACCATGGGCTCCGTGCCACTTCACTCCCATATTCTTCATCACGCTGCTGGTTCTGGGCAG 2531

Qy  2742 GCAGGTGGAGTCGACTGCCGCTGGAAACTTCCTCTGGAAACTACAGGCACAGGGGAGAA 2801
         | ||| | ||||  |||| || || |||||| |||  |||| |||| |||
Db  2532 ACAGAGTGAATATTACTGTAGGTTAGACTTCTTGTGGAGAACAAGTCAAAAAAGAGACG 2591

Qy  2802 GGAGGAGATGAGGAGGCTACAGCGATCACACCGGAGGCTGCTGCATAACATTCTGCCCAA 2861
         |||||||||||  |||  || ||  | ||| ||||| |||  ||  ||||| ||| |
Db  2592 GGAGGAGATAGAAACCATGGAGAACCTAAATCGAGTGGCTGCTGGAGAAACGTGCTTCCTGC 2651

Qy  2862 GGACGTGGCGGCCCACTTCCTGGCCCAATGATGAGACGCCCCAATGATGAACTCTACTATCAGTC 2921
         || ||| | ||| || ||||| |||| |||  | |||||   ||| || | ||  ||  ||  ||||
Db  2652 ACACGTGGCTGCTGGAACACTTCCTGGCCAGGAGGCTGAAAAATGAGGAGCTGTACCACCAGTC 2711

Qy  2922 GTGTGAGTGTGTGGCTGTTATGTTTGCCTCCAATTGCCAACTTCTCTGAGTTCTATGTGGA 2981
         || ||| || || ||||| || |||||| || | ||||||| |  || |||||  |||| |||
Db  2712 CTACGACTGTGTCGTGTGTCATGTTTGCCTCCATTCCGGACTTCAAGGAGTTCTACACAGA 2771

Qy  2982 GCTGGAGGCAAACAATGAGAATGATGGCTGCCTGGCCGCTGGCGCTGTCAACGGAGATCATCGCTGA 3041
         | ||| ||  ||| || ||| |||||| ||||  ||   || |  |||  || |||||  ||| |||
Db  2772 GTCAGATGTGAACACAGGAAGGCTTGGAATGCCTGGCGCTCCTGAATGAGATCATTGCTGA 2831

Qy  3042 CTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCACGTGAAAAGAGATCAAGACGATTGG 3101
         ||||||| || ||  ||  |||||  |   ||| | | |||  ||  || ||| |  || ||
Db  2832 CTTTGATGATCTGCTTTCTAAGCCAAAGTTCAGTGGTGTTGTTGAAAAGGATCAAGACCATTGG 2891

Qy  3102 TAGCACCTACATGGCTGCCTTCAGGGCTGACACGCGATCAGGTTGGGC------ 3157
         || | |  || | ||  ||  || | || || | || |||| || ||
Db  2892 GAGCACATACATGGCAGCCCACGGGACTGAGTGCCATACCCAGCCACGCGCCAGGA 2951

Qy  3158 ---------GCTCCCACATCACTGCCCTGCCTGACTACGCCATGCGGCCTCATGGA 3203
                  |||||  ||| || || || |||||  ||||| |||| || || |||
Db  2952 ACCTGAGCGTCAGTACATGCACATAGGCACCATGTGGAGTTTGCATATGCCCTGGTGGG 3011

Qy  3204 GCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTTCAGATGAAGATTGGGGCTGAA 3263
         |||||| || ||| ||||| ||| | || |||||| ||| |  |||  | || ||  ||
Db  3012 AAAACTGGATGCCATCAATAAGCACCTTCAACAGACTTCAAACTGCGAGTGGGTATCAA 3071

Qy  3264 CATGGGCCCAGTCGTGGCAGTGTCATCGGGGCTCGAAGCCACAGTATGACATCTGGGG 3323
         ||||| |  ||| |||   || |  ||  || |||| | || ||  || ||| || ||
Db  3072 CCATGGGCCTGTAATAGCTGGCGTCATAGGGGCTCAAAAAGCCACAGTATGACATCTCGGGG 3131

Qy  3324 GAACACAGTGAAATGTCTTCAGTCGTCGTATGGACAGCAGCGGGGTCCCGACCGAATCCAGGT 3383
         || || |||| | || |   ||  | |  | || |||| |  || || ||  ||||||| |||
Db  3132 CAACACTGTCAACGTGGCAGCGAATGGACAGCACCGGGGTCCTGCAACAAAATACAGGT 3191

Qy  3384 GACCACGGACCCTGTACCAGGTTCAGCTGCCAAGGGTGTCGAGGGGT 3443
         || ||| || | | |  |||| |   || |||| | || |||||| |
Db  3192 GACTGAGGAGACAAGCCTCATCTTGCAGACGGCTTGGCTACGACTGGTACACGTGCGAGTGTAT 3251

Qy  3444 GGTCAAGGTGAAGGGCAAGGGGGAGAATGACCACCTACTTCCTCAA 3488
         || ||  || || |  ||  |||| | | |  ||| |||||
Db  3252 CATCAATGTGAAGGGAGGGAAAGGGACCTGAAGACATATTTGTAAA 3296
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```
RESULT 13
US-08-726-214-3
; Sequence 3, Application US/08726214
; Patent No. 6107076
;  GENERAL INFORMATION:
;    APPLICANT:  Tang, Wei-Jen
;    APPLICANT:  Gilman, Alfred G.
;    TITLE OF INVENTION:  SOLUBLE MAMMALIAN ADENYLYL CYCLASE
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
```

```
Qy  1605 TGGCCAGCGCAACGCGTACCTTCAAGGAGCAGCACATTGAGACTTTTCCTCATCCTGGCGC 1664
         |||  |  |   | ||    || ||||| |||||||  || |||  |  | |||  || |
Db  1404 TGAGATAAGAGAGCACCCCATTATTAAAGCAGCACTTGGTGAAAACCTACTTTGTAATCAATCC 1463

Qy  1665 CA------GCCAGAAAACGGAAAGACGAGGAGAAGAGGCCATGCGCAGCCGCTGGCCAAGCTGCGGGGC 1721
         ||      |||| |||| || ||| | |||||| ||||| |
Db  1464 CAAGGGAGACGGAGACCGAGTCCTCAGCATCTCTTCAGACCTCGACACACTCTGGACGCAGAGC 1523

Qy  1722 CAACTCCATGAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCCTGGACCAA 1781
         || ||| || |  ||||    |  ||  |||   | |||  || |||  ||
Db  1524 CAAGATGAGAGCATCGTGTCGCCGTACCCGTGGTCCTGGGAGTCCTTGGGGAGCAGCCAAGCC 1583

Qy  1782 GGACTCCAAGGCCTTCCGCCCAGGATGGCATTGATGATTCCAGCAAAGACAACCGGGGCAC 1841
         |||  ||| |||  || |||| || |  | |||  |||  ||| | || |  ||| ||
Db  1584 ATTCGCACATCTGCACCAGAGATATGCATGACCACAGAGAATGGGAAGATTAGTACCAC 1643

Qy  1842 CCAAGATGCCCTGAACCTGGTCAACATAATGTTGATGAGTTCCTGCCGTGCCATCGATGC 1901
         ||| || |||   || || | || ||    || | ||||| ||  || ||  | |||  |
Db  1644 GGATGTGCCAATGGGTCAACTAATTTCAAATCGCACCTTAAGAACTAAGTCACAGAA 1703

Qy  1902 CCGCAGCCATTGATCAGCTGCCGGAGGACCATGTGCCCGGTTTCTGTCACCTTCCAGAG 1961
         || || || |||| | | || || || ||||||  ||  |||| ||| | | |||||
Db  1704 GAAGAGAGATTTGAAGAAGAACTGAATGAAAGGATGATCCAAGCAATTGATGGGATCAATGC 1763

Qy  1962 AGAGAGATCTTGAGAAGAAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCCTACGTTGC 2021
         |||| | | || ||| | |  || || || | || ||  ||  ||   || | | |
Db  1764 ACAGAAGCAATGGCTCAAGTCAACAAGTCAGTGGTGTTGAAAGGATCAAGAACAA 1823

Qy  2022 CTGTGCCCTGTTGGTCGTCTTCATCGTCATCTTCCAGCTTCATCATCTTCCCACACTC 2081
         ||  |  || |  |   || |||| ||   ||||||| ||||| || || | || |
Db  1824 GAATATAGAGAAAGAATACCGAGCTACTGACGTACTACGTGACCTG 1883

Qy  2082 CACCCTGATGTCTTGGGATCTATGCCAGCATCTTCCTGCTGCTGTCTAATCACCGTGCTGAT 2141
         || | || || | ||||  | | || ||  | |  | |  || | | || | | ||
Db  1884 TGCCTGCTCCATCTTTCTGCATCTTCATTGTACGATATCTGTATTGCCAAAAACGTC 1943

Qy  2142 CTGTGTGTGTACTCCTGTGTTCTCTGTGTTCCCTAAGGCCGTGCAACGTCTGTCCCGCAG 2201
         || | | | || || || | ||   ||  || | || | | || || |  |  | ||
Db  1944 CATCCTTGGCTTCTCTCCCTTTTGGAGCTGCATTTCTCTCCCTCATCCTCTTGTCTG 2003

Qy  2202 CATTGTCCGCTCACACATAGCACCCAGTTGCATCTTTTCCGTCCTCGCTGCTGTTGTT 2261
         | | || ||   || | |  ||||| | || |||  ||||  | |  || | |
Db  2004 CTTCGCTGGACAGCTTTTGCAATGCAGAGAAAAGGCCTCCACCTCTCTCATGTGGCTTTTT 2063

Qy  2262 TACTTCTGCCAACATGTTCACCTGTAACCACACACCCCATAGGGAGCGTGTGCAGC 2321
         || | ||||| || | | |  |||    || ||| ||  | |  |||  |
Db  2064 GCATCATCGCCAACCGCCAACCGCCCCATGGCCACGGATCTCCCTCAC 2114

Qy  2322 CCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGCCACCTGTCAGCAGCTCAATTA 2381
         || || | | || ||| | | |||  ||||| ||  || || |||| | ||| |  |||
Db  2115 AATCGTCACCACGGCTATCATACTAACCATGGCTGTGTTCAACATGTTTTTCCTGAGCAA 2174

Qy  2382 CTCTCTGGGCCTCGGATGTCCTGGATGTCCCCGTGTGAGGGCACCATGGCCCACCTGTTCCTGA 2441
         | | ||| || | ||   | |||    ||
Db  2175 CTCTGAGGAGACAACCCTTCCCACTGCCAATACACTGCCAATACATTACATCAAATGCAAACGTTTCTGTCTGCCGGA 2234

Qy  2442 GTACTTCATCGGGAACATGCTGCTAGTGCTCTTGGCCAGCTCGTCTTCCTGCACATCAG 2501
         |  ||| |  || ||||||  || || ||  | | ||||
Db  2235 TAACCAGGCGTCGAAGTTGCATGCTCGATGCTTGTTTTCCTCCCGGCTACTTCATCATACAG 2294

Qy  2502 CAGCATCGGGAAGTTGGCCATGAATGTCTTTGCTCCTGCTTGGGGCTCATCTATTTGGTGCTGCTTCT 2561
         ||  || | |||  |  || | | ||  | | || |
Db  2295 CTGCATCCTGGGCTTCATCGATCCTGTCCGTTTCCTGAGGGTGAACTATGAGTTAAAAAT 2354

Qy  2562 GCTGGGTCCCCAGCCACCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTT 2621
         || ||  | |||| || ||  ||  | | | || ||  | ||   ||| |||||
Db  2355 GTTAATCATGATGGTGCACTCGTGGCGACTACAACACCATTCTACTTCCACACCCATGCC-- 2412

Qy  2622 GGCTCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGCTGCAGAGGAGGGTGCCCT 2681
         |||  | |   |||  | | | ||  | ||  || ||  | ||  ||
Db  2413 -CATGTTCTGGATGCCGATGCCTACAGCAGCCAGTCCTGTTTCAGAGACGCCATTGGAAAGAGACCT 2471
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ZIP:  77210
COMPUTER READABLE FORM:
  MEDIUM TYPE:  Floppy disk
  COMPUTER:  IBM PC compatible
  OPERATING SYSTEM:  PC-DOS/MS-DOS
  SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER:  US/08/726,214
  FILING DATE:  Concurrently Herewith
  CLASSIFICATION:  435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:  US 60/005,498
  FILING DATE:  04-OCT-1995
ATTORNEY/AGENT INFORMATION:
  NAME:  Highlander, Steven L.
  REGISTRATION NUMBER:  37,642
  REFERENCE/DOCKET NUMBER:  UTSD:450
TELECOMMUNICATION INFORMATION:
  TELEPHONE:  (512) 418-3000
  TELEFAX:  (512) 474-7577
INFORMATION FOR SEQ ID NO:  3:
SEQUENCE CHARACTERISTICS:
  LENGTH:  4008 base pairs
  TYPE:  nucleic acid
  STRANDEDNESS:  single
  TOPOLOGY:  linear
US-08-726-214-3
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Query Match       12.9%;  Score 458.6;  DB 3;  Length 4008;
Best Local Similarity  50.1%;  Pred. No. 1.8e-101;
Matches 1346;  Conservative   0;  Mismatches 1279;  Indels   60;  Gaps   6;
```

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TITLE OF INVENTION:     ADENYLYL
TITLE OF INVENTION:     CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
NUMBER OF SEQUENCES:    6
CORRESPONDENCE ADDRESS:
   ADDRESSEE:  Brumbaugh, Graves, Donohue and
   ADDRESSEE:  Raymond
   STREET:     30 Rockefeller Plaza
   CITY:       New York
   STATE:      New York
   COUNTRY:    U.S.
   ZIP:        10112-0228
COMPUTER READABLE FORM:
   MEDIUM TYPE:       Floppy disk
   COMPUTER:          IBM PC compatible
   OPERATING SYSTEM:  PC-DOS/MS-DOS
   SOFTWARE:          PatentIn Release #1.0,  Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER:   PCT/US95/11808
   FILING DATE:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER:   US 08/307,896
   FILING DATE:          16-SEP-1994
ATTORNEY/AGENT INFORMATION:
   NAME:                 Clark, Richard S.
   REGISTRATION NUMBER:  26,154
   REFERENCE/DOCKET NUMBER:  29970 165/28755
TELECOMMUNICATION INFORMATION:
   TELEPHONE:  (212) 408-2500
   TELEFAX:    (212) 765-2519
   TELEX:      650 6111063
INFORMATION FOR SEQ ID NO:  5:
SEQUENCE CHARACTERISTICS:
   LENGTH:       4008 base pairs
   TYPE:         nucleic acid
   STRANDEDNESS: single
   TOPOLOGY:     linear
   MOLECULE TYPE:  cDNA
PCT-US95-11808-5

Query Match    12.9%;  Score 458.6;  DB 5;    Length 4008;
Best Local Similarity  50.1%;  Pred. No. 1.8e-101;
Matches 1346;  Conservative  0;  Mismatches 1279;  Indels  60;  Gaps  6;
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Qy     852  CCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTCCTCGTGTCTCCTGCCACCAAGTCATTGGCAT  911
            ||||||    |||||||||||||||||||||| ||| | |||||||||||||||||||||||||||||
Db     624  CCTGTTCTGGCAGATACTGGCCAATGTGATCATTTGGGAACTTCGGCGGGAGC  683

Qy     912  CTGCACACATCCAGCAGAGGGTGTCAGCAGCTTGCCTTGCCATGACAAACCTATCGGAGGACCCGGTTA  971
            || ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     684  CTACCACAAGCACCTCAGCGAGCTTGCCTTGCCATGACAAAGCCAGCAGGAGGCGGCTCGTGCTGTC  743

Qy     972  CATCCAGGCCCCGGCTCCACCTGCAGCATGGAATCGGCAGCAGAATCGGCAGCAGGAGCGGCTCGTGTC  1031
            || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     744  CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAACGGCAGCAGGAACGCAGCCTCCTGCTCTC  803

Qy    1032  GGTATTGCCCCAGGCAGCACGTTGCCATGGAGATGAAGAAGACATCA-----------A  1076
            ||||||||||||| |||||||||||||| ||||||||||||||||||            |
Db     804  CTTGCTGCCAGCTCACATCGCCATGCCATGGAGATGAAGAAGCTGAAATCATTCAGAGGCTGCAGGG  863

Qy    1077  CACAAAAAGAGAGACATG-------ATGTTCCACAAGATCTACATACAGAAGCA  1124
            |||||||||||||||||         |||||| ||||| |||| |||||||||||
Db     864  CCCAAAGCAGGACAGATGGAGAAAACAAACAACTTCCACAATTCCACAATTCCACAATCTCGTGTATGTCAAACGACA  923

Qy    1125  TGACAATGTCAGCATCCGTTTGCAGACATTGAGGGCTTCACCGGGTTCACCAGGTCCAGTG  1184
            ||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     924  CACCAAGTGAGCAATGTGACCATCCAGCATTATACGTCACATTGTGGCTTCACCGGGTTG  983

Qy    1185  CACTGCGCAGGAGCTGGTCATGATGACCCTGCAATGAGCTCCTTTGACAAGCTGCTGC  1244
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     984  CTCCCCTGGCAGCTCACATGCTCCACATGCTGAATGAACTCTTTGGGAAGTTGATCAAATAGC  1043

Qy    1245  TGCGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGG  1304
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Db    2295  CTGCATCCTCGGGCTTGATCTCTGCTCCGTTTTCCTGAGGGTGAACTATGAGTTAAAAAT  2354
            |||||    |||||||||||| |||||||||||||||||||||||||||||||||||
Qy    2562  GCTGGGTCCCCAGCCACCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTT  2621

Db    2355  GTTAATCATGATGGTGCACTCGTCGTGGCTACAACACCATTCTACTCCACACCCATGCC--  2412
            |    ||||||      |||||     |||||||||||||||| |||||||||||||||
Qy    2622  GGCTTCTTCCAATGAGACCCTTGATGGGCTGGACTGTCCAGCTGTCCAGCTGAGGGGTGCCCT  2681

Db    2413  -CATGTTCTGGATGCCTACAGCCAGGTCCTGTTTTGCAGAGACCAGCCATTGGAAAGACCT  2471
             |||  |||||||||       |||||| |||||  ||||||    |||||||||||||||
Qy    2682  CAAATATGACCCCTGTGATTCTGCTGGTGTTTCGCTGCTGCGCTGTATCTGCATGCTCA  2741

Db    2472  GAAGACCATGGGCTCCGTGCACTCTCCATATTCTTCATCACGCGTCTGGTTCTCGGCAG  2531
            |||||||||||||    |||  |||||||||||||   ||||||||||||||||||
Qy    2742  GCAGGTGGAGTCGACTCGCCCGCCTAGCTTCCTCTGGAAACTACAGGCAACAGGGGAGAA  2801

Db    2532  ACAGAGTGAATATTACTGTAGGTTAGACTTCTTGTGGAAGAACAAGTTCAAAAAAGAGCG  2591
            |||||||||| | |||||     ||||||||| ||||||||   ||| |||||||||||
Qy    2802  GGAGGAGATGGAGAGGAGCTACAGGCATCAACCGGAGGCTGCTGCATAACATTCTGCCCAA  2861

Db    2592  GGAGGAGATAGAAAACCATGAGAAATCGAGTGCTGCTGCTGGAGAACCTGACGCTTCCTGC  2651
            |||||||||  |||||||||||| ||||||||||||||||||  ||||||||||||||||
Qy    2862  GGACCTGGCCGCGCCCACTTCCTGGCCCGGAGCGCGCCGCAATGAGAACTCTACTATCAGTC  2921

Db    2652  ACACGTGGCTGAACACTTCCTGGCCCAGGAGCCTGAAAATGAGGAGCTGTACCACCAGTC  2711
            |||||||||||||||||| |||||||||||||| ||||||||||||||| ||||||||||
Qy    2922  GTGTGAGTGTGTGGCGTGTTATGTTTGCCTCCATTGCCCAACTTCTCTGAGTTCTATGTGGA  2981

Db    2712  CTACGACTGTGTCTGTGTCATGTTTGCCTCCATTCCGGACTTCAAGGAGTTCTACACAGA  2771
            ||||||||||| |||||||||||||||||||||||||||||||| ||||||||| | ||
Qy    2982  GCTGGGAGGCAAACAATGAGGGTGTCGAGTGCTGCTGCTGCTCACGAGATCATCCTGA  3041

Db    2772  GTCAGATGTGAACAGGAAGGCTTGGAATGCTGGCGGGCTCCTGAATGAGATCATTGCTGA  2831
            |||||| |||||||||||||||  |||||||||||||||||| ||| |||||| ||||||
Qy    3042  CTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAAAGATCAAGACGATTGG  3101

Db    2832  CTTTGATGATCTGCTTTCTAGCCAAAGTTCAGTGGTGTTGAAAAGATCAAGACCATTGG  2891
            ||||||||||  ||| |||| |||||| ||||| |||||||||||||||||||||||||
Qy    3102  TAGCACCTACATGGCTGCTCCTCAGGGTGAACGCGGTGAACGCCACCTACGATCAGTGGGC-----  3157

Db    2892  GAGCACCTACATGGCAGCACATGGCAGCCACGGGCGACTGAGTGCCATACCCAGCCAGGAGCACGCCCAGGA  2951
            |||||||||| ||| ||| |||||||||||||||| ||||| ||||| |||| ||||| ||
Qy    3158  ------GCTCCCAATCACTCGGCGTGCCATCACTGGCTGAGTTTGCATCGCCCTGGTGGG  3203

Db    2952  ACCTGAGCGTCAGTACGACATCAATGACAAAGGCACCCTTCTTCAACAATTTCGAGATGGAAGATTGGGCTGAA  3011
            |||| |||  |||| |||||||| ||| |||||| |||| ||||||| ||||| |||||||||||
Qy    3204  GCAGATGAAGCACATCAATGAGCACTCTTCAACAATTTCGAGATGGAAGATTGGGCTGAA  3263

Db    3012  AAAACTGGATGCCATCAATAGACACTCCTTCAACGACTTCAAACTGCGAGTGGGTATCAA  3071
            |||| |||||| ||||||| ||||| | |||||||||| |||||||||||||||||
Qy    3264  CATGGGCCCAGTCGTGTGCAGGTGTCAGGCGTCGGAAGCCACAGTATGACATCTCGGGG  3323

Db    3072  CCATGGGCCTGTAATAGCTGGCGTCATAGGGGTCAAAAGCCACAGTATGACATCTCGGGG  3131
            ||||||||| ||||| |||| |||||||||||||||||||||||||||||||||||||
Qy    3324  GAACACAGTGAATGTCTTCTAGTCGTATGGACAGCAGAGGGGTCCCCGACCCAGGT  3383

Db    3132  CAACACTGTCGTCAACGTGGCCCAGGTTCTAGCTGCCAAGGGCATCGGAGGGTCGAGGGGT  3191
            |||||| ||  ||||||||||||||||||||  |||| |||||||   ||||||||||
Qy    3384  GACCACGGACCCTGTACCAGGTTCTGGCCAAGGGCTTGGCTACAGTGTCGAGGGGT  3443

Db    3192  GACTGAGGAGCAAGCCTCATCTTGCGAGACGTGTTGGCTACAGTGTACATGTCGAGGTAT  3251
            |||| |||  |||||| ||||| |||| ||| ||||||||||||||| ||||||||| ||
Qy    3444  GGTCAAGGTGAAGGGCAAGGGCAAGGGCAGTGAAGGGAACCTGAAGATCAATCCTACTTCCTCAA  3488

Db    3252  CATCAATGTGAAGGGGAAAGGGGAACCTGAAGGGACCCTGAAGCATATTTGTAAA  3296
            |||||| ||||| |||||| |||||||||||||  ||||||||||||||| ||||
Qy    3264  CACCAAGTGAGCAATGTGACCATCCAGCATTATACGTCACATTGTGGCTTCACCGGGATTG  3296
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```
RESULT 14
PCT-US95-11808-5
; Sequence 5, Application PC/TUS9511808
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Srinivas Ravi V.
; TITLE OF INVENTION: MUTANT ACTIVATED GsALPHA AND
```

This page contains a nucleotide sequence alignment (Query "Qy" vs Database "Db") with positional numbering. The sequence data is presented in two blocks of paired alignment rows with base-pair match indicators (|).

(Left block, paired Db/Qy rows with coordinates ranging 1044–2381)

(Right block, paired Db/Qy rows with coordinates ranging 2115–3443)

Qy   3444 GGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCCTCAA 3488
                 |||||||||| |||| ||||| |||||||||||| |
Db   3252 CATCAATGTGAGGGGATGGGAGGGACCTGAAGACACATATTTTGTAAA 3296

RESULT 15
US-09-016-434-1344
; Sequence 1344, Application US/09016434
; Patent No. 6500938
GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/016,434
;   FILING DATE: HEREWITH
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1344:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2731 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g349268
US-09-016-434-1344

Query Match   12.8%;   Score 456.2;   DB 4;   Length 2731;
Best Local Similarity 52.8%;   Pred. No. 5.6e-101;
Matches 1274;   Conservative 0;   Mismatches 1023;   Indels 114;   Gaps 9;

Qy   1090 GACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGACATCCTGTTTGCA 1149
                 ||||| ||| ||||||||| | |||| |||||||| ||||||||| |||||||||||
Db   24 GAGAGGATTTTTCCACAAGATTTACATCCAGAGAGCACACAATGTGAGCATCCTGTTTGCT 83

Qy   1150 GACATTGAGGGGCTTCACCAGCTGCCATCCTGGCATCCCAGTGCACTGCACTCGTCAGACC 1209
                 |||||| ||| ||||||||||| || ||||||||| ||| || |||| |||| |
Db   84 GACATCGTGGGTTTCACGGGGCTTGGCATCCCAGTGCACGGCGAGAGAGCTGGTGAAACTC 143

Qy   1210 CTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCCTGAGGATC 1269
                 || ||||||||| |||| | ||| ||| ||| |||| || | |||| ||| |||
Db   144 CTCAATGAGCGCTTCGGCAAGTTCGATGAGTTAGCCACGAGAACCACTGTCGCGCCGCATC 203

Qy   1270 AAGATCTTGGGGGACTGTTACTACTGGTGTGCTCTACTGCGGTGTGGGGCCCGGCGACCAT 1329
                 |||||||| |||||| | | |||| | |||||||||||||||| ||| ||||
Db   204 AAGATTCTCCACAAGATCGCTACTCGGTGTGCTACTACTCTCTGGGGCCTTGGCTGCCACAT 263

Qy   1330 GCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGTGTACGTGAG 1389
                 ||||||||||||| ||||| ||||| ||| ||| |||||| || | |||||| |
Db   264 GCCCACTGCTGTGTGGAGATGGGGACTGACATGATTGATACCATCACATCGTGGGCTGAA 323

Qy   1390 GTGACAGGTGTGAATGTGAATCTGAACATGCGGCTGGGCATCCAACAGCGGCGGCTGCACTGC 1449
                 |||| | || || | | || ||| | ||| | |||| | ||| ||||| |||
Db   324 GCCACCGAGTGGATCTGAACATGCGTGTGGGTCTGCACACGGCAGGGTCCTCTGTGGT 383

Qy   1450 GTCTTGGCTTGCGCAAGTGGCAGTTGCAGTACGACGTGTGGTGTGCAATGATGGACCCTGGCCAAC 1509
                 ||||||||| |||||||||||||| | | | |||||||||||| ||| | |||| ||||||
Db   384 GTCCTCGGGCTTGCGCAAGTGGTGTTGCCAATGATGTGACCTTGGCCAAT 443

Qy   1510 CACATGAGGGACTACGAGGTGGAGCCAGGCCGTGGTGGCGAGCCGCAACCACGCGTACCTCAAG 1569
                 |||||||||| ||||| || |||| ||| | ||| || |||||| || || |||||||||||
Db   444 GTCATGGAAGCGCCGCTGCCTGCTGCAGGGAAGGTTCATATCACAAAGACACCCCAGCCGTGC 503

Qy   1570 CTGAACGGGGACTACGAGGTGAGCTGGAGCCGGTGGTGGGCGAGCCCAACTCCCATGCGCGAAAGATATTTCCAGGC 1629
                 ||| ||| |||||||||||| ||| ||||| ||||| | | | ||| | | || ||| ||| | |||||||
Db   504 TTGAATGGGGACTACGAGGGTAGAACCGGGTTACGACAATGGTTACAGAGGGATTCAAGATATTTCCAGGC 563

Qy   1630 GAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCGCAGCCCAGCAACGGAAAGATATTTCCAGGC 1689
                 ||||||| || ||| | | ||| | | |||| |||||| | || |||||||||||| |||||
Db   564 ACTCATACAATCGAAACCTTTTTATTGTGCCATCCCATCCCGGAAAAGATATTTCCAGGC 623

Qy   1690 GCCATGCTGGCCAAGCTGCAGGCGACTCGGCGGCCAACTCCATCGGAAGGGCTGATGCCGCGC 1749
                 |||||| | ||||||||||| | | | ||| | ||| || ||||| ||||||||||
Db   624 CTGATTCTTCTCAGATATAAAACC------GGCAAAAGGATGAAGTTCAAGACTGTCTGC 677

Qy   1750 TGGGTTCCTGATCGTGCCTTCTCCCCGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGC 1809
                 ||| ||||||||| | |||| ||||| ||||||| || ||||| |||||| |||||||||
Db   678 TACCTGCTGTGTGCAGCTCATCGACACTGCCCGGAAAATGTTCAAGGCCGGAGATCCCCTTCTCC 737

Qy   1810 ATTGATGATTCAGCAAAGACAACACCGGGGCACCCAAGATGCCCAAGCGGATGAG 1869
                 || | ||||||||||| | ||| | | || | | | || |||||||||
Db   738 AATGTCATGACCTGCGAGGACGA----------------TGACAAGCGCGAGGGC 775

Qy   1870 GTGGATGAGTTCCTGAGCCGTGCCATCGATGCCGCGAGCATTGATCAGTCGTCGGGAAGGAC 1929
                 || | | ||| | |||| ||||| | | | ||| |||| | || |||| |
Db   776 ATTAAGAACAGCTCCGGAAAACTCAGAAACCGCTCATCTTTTCTACCAACG------ 828

Qy   1930 CATGTGGCCGGTTTCTGCTCACCTTCCAGAGAGGATCTGAGAGAAGTACTCCCGG 1989
                 ||||||||| |||||| || ||||| ||||||| || | | | || ||||||
Db   829 --------------TTGTCTACACCACCCGGGCACTCGCGTCAACAGGTACATCAGCCGC 875

Qy   1990 AAGGTGATCCCCGCTTCGGAGCCTACGTTGCCTGTGGCCTGTTCATC 2049
                 ||| ||| | || || | | | |||| | |||||| |||
Db   876 CTCTTAGAAGCCGCCGCCAGAGCAG---AGCTGGAGGATGGCAGACCTGCAGCGAACTCTTTTACCCTG 932

Qy   2050 TGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATGCTTGGGATCTATGCCAGC 2109
                 ||| | | || | | |||||||||| || || | ||||| | ||||||||||
Db   933 AAGTACAAACATGTCGAACGGGAGCAAAAGTACCACCAGCTTCAGGACGAGTATTTCACC 992

Qy   2110 ATCTTCCTGCTCGTGCTCGTGCTAATCACCGTGCTAATCGATCGTGCTGTCCTGTCGTTCTG 2169
                 ||||||||| ||| || || || | | || || ||| | | ||| |
Db   993 AGCGCCGGTTGTCCTCACCCTCACCCTATCTGGCTGCCTTATTTGGCCTTGTTCTACCTTCTAATA 1052

Qy   2170 TTCCCTAAGGCCCTGCAACGTCGTCCGCAGCATTGTCCGGCTCACGGGCACATAGCACC 2229
                 ||||| | || ||| | |||| | || |||| | || | |||| | ||||||||||
Db   1053 TTCCCACAGAGTGTGGTCGTCGTGCTTCCTGCTAGTATTCTGAGCATCGTTCCTGGTGGCC 1112

Qy   2230 GCAGTTGGCATCTTTTCCGTCCTCGTTGTTTACTTCTCTGCCAACATGTTCACC 2289
                 ||| | || | ||| || | | | | || || |
Db   1113 TGTGTCCTGTACCTGCACATCACCCCGGGT------CCAGTGTTTTCCAGGGTGCC 1161

Qy   2290 TGTAACCACACCCCCATACGAGCTGTGCAGCCCGATGCTGAAACTGTCAGCCCGAGGATC 2349
                 | | | || | | | | || || |||| || ||| || || ||||
Db   1162 TGACGATTCAGATTCGCCACTGTCCTGTGATTTCATAGTGGTCTTAATCTACTCAGTAG 1221

Qy   2350 ATCACTGCCTGCCACCTGCAGCGCTCAATTACTCTCTGGGGCCTTGGGCCTGGAGCTGTGT 2409
                 || || | ||||| | ||||| | || |||| ||||| |
Db   1222 CCCAAGG------TTGTGTGGTGGCGCTGCCGCCTTGGCCGCTGCCTTGGGCCTGGAGACTGACCAT 1271

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Db    2319 TTTCTAGAAGG 2329
               ||| ||  | ||
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Search completed: January 7, 2004, 07:42:02
Job time : 250 secs

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Qy 2410 GAGGGCACCATGCCCACCTGCCAGCTTCCTGAGTACTTCATCGGGAAACATGCTGCTGAGT 2469
                   |    ||                           |    |||     |
Db 1272 AACAGTTCCCTGGTGTCCTTTCGTCTGGGGCCCAGCGCACAGCCCTGCCCACCCTGCCC 1331

Qy 2470 CTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGGAGTTGGCCATGATCTTT 2529
                  ||            ||            |  | |
Db 1332 TGCGAGTCTACACACCATGCCCTGCTCTGCTGCCTGGTGGGCACCCTCCCGCTAGCCATA 1391

Qy 2530 GTCTTGGGGGTCATCTATTTGGTGCTGCTTCTCGCTGGGTCCCCAGCCACCATCTTTGAC 2589
             |  | |||   |                   ||
Db 1392 TTTTTCCGGGTGTCCTTGCCAAAAATGATCCTGCTCTCCGGGCTCACCACGTCCTAC 1451

Qy 2590 AACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGG 2649
               || |  |   |||||  |
Db 1452 ATCCTCGTTCTGGAGCTCAGCGGATACACCAGGAC------------------------ 1486

Qy 2650 CTGGACTGTCCAGCTGCAGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTG 2709
                |       ||  |||  ||             |
Db 1487 -------TGGGGGTGGTGCCGTCTCCGGGCGCAGCTACGAGCCGATTGTGGCCATCCTG 1538

Qy 2710 GTGTTGCGCGTGGCGCTGTATCTGCATGCTCAGCAGGTGGAGTGACTGCCCGCCTAGAC 2769
              |||||  || |||                ||||||  |       ||
Db 1539 CTCTTCTCCGTGTGCGCTGCCCTGCCATGCCAGGCAGGTGGACATCAGCGTGGAGGCTGGAC 1598

Qy 2770 TTCCTCTGAAAACTACAGGCAACAGGGGAGAAGGAGGAGGATGAGGAGGAGCTACAGGCATAC 2829
           |||| |        ||||| |     ||| ||       |   |||   ||||  |
Db 1599 TACCTTCTGGGCGCCACAGGCAGGAGGCAGGAGGACATGGAGAAGGTGAAGCTGGAC 1658

Qy 2830 AACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGCGCCCACTTCCTGCCCGG 2889
           | |  |   |  ||||       ||||| |||          |    ||
Db 1659 AACAGGGCCATCCTCTTCAACCTCCTGCCCAGCACTTCCTCATGTCC 1718

Qy 2890 GAGGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCGTTATGTTTGCC 2949
           | | |  || ||      ||||  ||||| |       | |||   ||||||||||
Db 1719 AACCCCTCGGAACATGGACCTTCTACTACCAGTCCTACTCCCAGGTGGGGCGTCATGTTTGCC 1778

Qy 2950 TCCATTGCCAACTTCTCTGAGTTCTTATGTGGAGCTGGAGCCAAACAATGAGGGTGTCGAG 3009
           |||||  |||||| |  ||   || |||  ||||||| ||||   |||||  || |||||
Db 1779 TCCATCCCCAACTTCAATGACTTCTCAATGACTTCTACATCGAGCTGGACGGCAACAACATGGGGGTGGAG 1838

Qy 3010 TGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGG 3069
          | |||||||||| ||||||||||||||| ||||||| | |||  |||  |||  ||  |
Db 1839 TGTCTGCGGCTTCTCAACGAGATCATCGCCGACTTTGACGAGCTCATGGAAAAAGACTTT 1898

Qy 3070 TTCCGGCAGCTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTG 3129
           |||  |  | ||||||||||||||| || || |||||||||||| || |  |||| ||
Db 1899 TACAAGGACATAGRAGAAGATCAAGACCATCGGGAGCACCTACATGGCCGCTGTGTGGGCTA 1958

Qy 3130 AACGCC--------AGCACCTACGATCCAGGTGGGCCGCTCCCACATCACTGCCCTGGCT 3180
          ||||||         |  | ||    | || |  ||   |||| ||   | ||| |||||
Db 1959 GCGCCACCTCGGGGACCAAGGCTAAGAGAGTCCATCTCCTCCCCACCTGAGCACGCTGGCG 2018

Qy 3181 GACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240
          |||| |||||| |   ||    ||| |||||| |||| ||| |       | ||||||||
Db 2019 GACTTTGCCATTGAGATGTTTGACGTTCTGGATGAAATCAACTACCAGTCTTACAACGAC 2078

Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTCGTGGCAGGTGTCATCGGGGCTCGG 3300
           || |  | ||| ||||| | | |  ||||||  |||| | ||| ||    |||| |||| |||
Db 2079 TTTGTCCTCCGAGTTGGCATCAATGTTGGCCCTGTGGTTGGCTGGAGTGATTGGCGCTCGC 2138

Qy 3301 AAGCCACAGTATGACATCTGGGGGAACAACAGTGAATGTCTCTAGTCGTATGACAGCACG 3360
          |||||||||||||||||||||||| |||||||||| |    ||| ||  ||||| |||||
Db 2139 AGGCCCCAGTACGACATCTGGGGAAACACACAGTCCAGTCGGATGGATAGCACA 2198

Qy 3361 GGGGTCCCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGC 3420
          ||||||| | ||| ||||||||||||| |||    | |  ||| ||    ||||| ||||
Db 2199 GGGGTCCAGGGCAGAAATCCAGGTGACTGACGGAAGTCCACCGGCTGCCTGAGAAGGTGCCCC 2258

Qy 3421 TACCAGCTGGAGTGTGAGGGGTCGGTCAAGGTGAAGGGCCAAGGGGGAGTGACCACCTAC 3480
          |||||  |||||||| || || | ||||||||||||||||||  |||| ||  |||| ||
Db 2259 TACCACTTTGTGTGCCGAGGCAAAGTCAGTGTCAAGGGCAAAGGCGAGATGTTGACATAC 2318

Qy 3481 TTCCTCAATGG 3491
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